



10724598  
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: BLANCHE, FRANCIS; CAMERON, BEATRICE; CROUZET, JOEL; DEBUSSCHE, LAURENT; LEVY SCHIL, SOPHIE; THIBAUT, DENIS

(ii) TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE BIOSYNTHESIS OF COBALAMINS AND/OR COBAMIDES, DNA SEQUENCES CODING FOR THESE POLYPEPTIDES, PREPARATION METHOD AND THEIR USE.

(iii) NUMBER OF SEQUENCES: 60

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER  
(B) STREET: 1300 I STREET, N.W.  
(C) CITY: WASHINGTON  
(D) STATE: DISTRICT OF COLUMBIA  
(E) COUNTRY: USA  
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: FLOPPY DISK  
(B) COMPUTER: IBM PC COMPATIBLE  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WORDPERFECT 5.1

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 10/724,598  
(B) FILING DATE: 01-DEC-2003  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/426,630  
(B) FILING DATE: 21-APR-1995  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/916,151  
(B) FILING DATE: 14-SEP-1992  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/FR91/00054  
(B) FILING DATE: 30-JAN-1991  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: S.J. ARRIGO  
(B) REGISTRATION NUMBER: 46,063  
(C) REFERENCE/DOCKET NUMBER: 03806.0050-02000

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (202) 408-4160  
(B) TELEFAX: (202) 408-4400

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5398 base pairs

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(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Pseudomonas denitrificans  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:

(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Nucleotide Sequence of the 5' to 3' strand from the 5398 bp *Clai*-*HindIII*-*HindIII*-*HindIII* fragment of *Pseudomonas denitrificans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGGCTGCAGG	TCGACTCTAG	AATCGATGAA	GCCTGCATG	AAGGCAGGCGA	CGAACAGGAA	60
GGCGAGCAGG	TGGAAGGCGA	GATCTTGCAC	GGCGGGACT	CGAGAGGAGA	GCTGTCAGGC	120
GGGATTTCC	GCCTTGTGTC	AGAGCCCGGC	GCGATTGCA	AAGCCTTCTG	TCGCGGTGTT	180
GCTGTCCATG	CAGGTGTCGA	AATTGAAAAA	CCGACAAAGA	TTCACAGCCT	TGTTCCAGCT	240
CGCTGTCTTT	CTGGATGGAG	GCGCTCTCGC	CCGCATGGT	CCGAAGAAGG	GCTGTCCTTG	300
CGATAACGGA	GGCGGATGAC	GATCTTCCTC	AAACGCGACA	TGGCGATGGC	GCAATCCGGT	360
TTGACCGGCC	TTCCCGCGCTC	CGGTAAAAAT	GAAGGATATG	CGACGGCGTC	CGCTTGGCG	420
GACTGAAAGA	GCGTCCCGGTG	CGGCCGACCC	AGTCAGGGGG	GCATCAGCCG	GTGCTGTCCA	480
GATCGGCCGG	GACGGATCGT	CCCAGCCGGC	GCTTCGTTAA	GGAGAACAAAC	GAAGGGAGCC	540
GGCCGCCGAT	GCCATCGGGC	CAACACTCTG	CACAGACGAC	GAAAGCAGGA	GCCGGGCTGG	600
TGCTCGGGCT	CGGCTGCGAG	CGTCGACGC	CGGCCGAAGA	GGTGATCGCC	CTTGGCCGAGC	660
GTGCGCTTGC	CGATGCCGGT	GTTGCGCCCG	GCGATCTCG	GCTGGTCGCC	TCGCTCGATG	720
CTCGGCCGA	GGAGCCGGCG	ATCCTGGCG	CCGCTCAGCA	TTTCGCGGTT	CCGGCCCGT	780
TCTACGATGC	CGCCACGCTC	GAAGCCGAAG	CTTCCCGGCT	CGCCAACCCG	TCCGAGATCG	840
TCTTTCGCTA	CACGGGTTGT	CATGGCGTTG	CCGAGGGTGC	AGCGCTCGTC	GGGCCTGGTC	900
GCGAAGCCGT	GCTGATTGTC	CAGAAGATCG	TCTCCGCCA	TGCGACGGCC	GCACTTGGCG	960
GGCCGGCGAC	CTTGCAGGCC	GAAAAGCGCA	TCCAGGCCGC	GGAGGCTGTC	TGATGCATT	1020
TTATTTGTT	GAATTGAATC	AATCTTTGC	CCGGGGTTTC	TCTCAAGTGG	AATCCGGTTC	1080
TTTAGAGAGC	GGCTCAGGGC	TGCCGTTGGG	TGGCGCCGAA	ATACAGGTGG	GACAGCACGC	1140
ATGATCGACG	ACCTCTTGC	CGGATTGCCG	GCGCTCGAA	AAGGTTCGGT	CTGGCTGGTC	1200
GGCGCCGGCC	CCGGCGATCC	CGGCCCTGTT	ACGCTGCATG	CGGCCAATGC	GCTGCCAG	1260
GCGGATGTGA	TCGTGCATGA	TGCGCTGGTC	AACGAGGATT	GCCTGAAGCT	CGCGCGCCG	1320
GGCGCCGTGC	TGGAGTTTC	GGGCAAGCGT	GGCGGCAAGC	CGTCGCCGAA	GCAGCGCGAC	1380
ATCTCGCTTC	GCCTCGTCA	ACTCGCGC	GCCGGCAACC	GGGTGCTGCG	CCTCAAAGGC	1440
GGCGATCCCT	TGTCCTTCGG	TCGCGGTGGC	GAGGAGGGCG	TGACGCTGGT	CGAACACCGAG	1500
GTGCCGTTCC	GAATCGTCCC	CGGCATCACC	GCCGGTATCG	GGGGCTTGC	CTATGCCGGC	1560
ATTCCCGTGA	CCCATCGCGA	GGTCAACACC	CGGGTCACCT	TCCTGACTGG	CCATGATTCC	1620
TCCGGCTTGG	TGCCGGATCG	CATCAACTGG	CAGGGCATCG	CCAGCGGCC	GCCTGTCATC	1680
GTCATGTACA	TGGCGATGAA	ACATATCGGC	GCGATCACCG	CCAACCTCAT	TGCCGGCGGC	1740
CGCTGCCCGG	ACGAACCGGT	CGCCTTCGTC	TGCAACGCCG	CGACGCCGCA	GCAGGGCGTG	1800
CTGGAAACGA	CGCTTGCAGC	TGCAAGAGGCC	GATGTTGCGG	CGGCAGGGCT	GGAGCCGCCG	1860
GCGATCGTCG	TCGTCGGCGA	GGTGGTGCAGG	CTGCGCGCAG	CGCTCGACTG	GATCGGCCG	1920
CTGGACGGGC	GCAAGCTTGC	CGCCGACCCG	TTCGCCAATC	GCATTCTCAG	GAACCCGGCA	1980

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TGAGCCGATT	GCTGATTGCC	GCACCCGGT	CCGGCTCCG	CAAGACGACG	GTGACGCTCG	2040
GGCTGATGCG	CGCCCTGAAG	AGGCGCGCG	TGGCGATCGC	GCCCCGCAAG	GCGGGGCCGG	2100
ACTATATCGA	TCCCCTTTTC	CACCGGGCAG	CGACCGGCGA	GCCCTGCTTC	AACTACGACC	2160
CCTGGCGAT	GCGCCCGGAA	CTGCTGCTTG	CCAATCGTC	GCATGTGGCC	TCCGGCGGGC	2220
GCACATTGAT	CGTCGAGGCG	ATGATGGGAC	TGATGACGG	TGCTGCCGAC	GGCTCGGGAA	2280
CGCCAGCGGA	CCTCGCCGCG	ACGCTGAACC	TTGCGGTAT	TCTGGTGGTC	GATTGCGCCC	2340
GCATGCCCCA	GTCGGTTGCC	GCCCTCGTGC	GCGGCTATGC	GGATCATCGC	GACGATATCC	2400
GGGTGGTTGG	CGTCATCCTC	AACAAGGTCG	GCAGCGATCG	GCATGAAATG	ATGCTGCGCG	2460
ATGCGCTCGG	CAAGGTGCGC	ATGCCTGTCT	TCGGCGTGT	CCGGCAGGAC	AGCGCATTGC	2520
AACTGCCGGA	GGGCCATCTC	GGGCTCGTGC	AGGCAGGGCA	ACACTCAGCG	CTTGAGGGCT	2580
TCATCGAGGC	GGCGGCCGCG	CGGGTCGAGG	CTGCTGCGA	TCTCGACGCC	ATCCGCTGA	2640
TCGCACGAT	TTTCCCAG	GTGCCCGCGG	CGGGCGATGC	CGAGCGTTTG	CGGCCGCTCG	2700
GTCAGCGCAT	CGCGGTCGCG	CGCGATATCG	CCTTTGCCTT	CTGCTACGAG	CACCTGCTTT	2760
ACGGCTGGCG	GCAAGGCGC	CGGGAGATT	CCTTCTTCTC	GCCGCTCGCC	GACGAGGGC	2820
CGGATGCGGC	AGCCGATGCC	GTCTATCTTC	CGGGGGTTA	TCCGGAGCTG	CATGCGGGC	2880
AGCTGAGCGC	CGCCGCCCGA	TTCCGTTCCG	GCATGCATT	CGCGGCGGAA	CGCGGCCGCC	2940
GCATCTTCGG	CGAGTGCGGC	GGCTATATGG	TGCTCGGCGA	AGGGCTTGTG	GCTGCCGATG	3000
GCACACGCTA	CGACATGCTC	GGCCTGCTGC	CGCTCGTAAC	CAGTTTGCC	GAGCGCAGGC	3060
GGCACCTCGG	CTATCGCCGC	GTCGTGCTG	TCGACAAACG	CTTCTTCGAT	GGACCCATGA	3120
CGGCGCACGA	ATTCCACTAT	GCGACCATCG	TCGCGGAAGG	GGCGGCCGAT	GGGCTGTTG	3180
CGGTCAAGCGA	CGCCGCCGGC	GAGGATCTCG	GCCAGGCCGG	CCTCCGGCGC	GGCCCTGTCG	3240
CCGGTTCTT	CATGCATCTG	ATCGACGTCG	CAGGTGCTG	ATGAGCGCAC	CGATGTTCA	3300
TGGTGGCGGC	ATCACCGAGG	CCGCGAGCGC	CTATGGCGG	CGGCGCTGAAG	ACTGGCTCGA	3360
TCTGTCGACC	GGCATCAATC	CATGCCCGT	CGCCTTGGCC	CGGGTCCCTG	AGCGCGCTG	3420
GCACCGGCTG	CCGGATCGGC	AGACGGTAGA	TGATGCGGG	AGCGCCGCCG	CCGACTACTA	3480
CCGCACCAAC	GGCGTGTGTC	CTTTGCCGGT	GCCGGGCACC	CAGTCGGTGA	TCCAGCTCCT	3540
GCCACGTCTT	GCTCCGGCCA	ACAGGCACGT	CGCGATTT	GGGCGACCT	ATGGCGAGTA	3600
TGCCCCGCTG	CTTGAAGCGG	CCGGCTTTCG	TGTCGATCG	GTCGCGGATG	CCGACGCGCT	3660
CACGGCCGAA	CATGGGCTTG	TCATCGTCG	CAACCCCAAC	AACCCGACCG	GCCGCGCTT	3720
GGCGCCGGCG	GAGCTTCTGG	CGATCGCCGC	AAGGCAGAACG	GCGAGCGGC	GACTGCTGCT	3780
GGTCGATGAG	GCCTTCGGCG	ATCTTGAGCC	GCAACTGAGT	GTCGCTGGTC	ACGCGTCAGG	3840
GCAAGGCAAC	CTCATCGTC	TCCGCTCTT	CGGCAAGTT	TTCGGCTTG	CGGGCCTGCG	3900
CCTCGGCTTC	GTCGTTGCGA	CCGAGCCAGT	GCTTGCATCC	TTTGCCTGATT	GGCTCGGTCC	3960
CTGGGCTGTC	TCCGGCCCGG	CGTTGACGAT	CTCGAAAGCG	CTGATGCAAG	GCGATACGAA	4020
GGCGATCGCG	CGGGGCATCC	TCGAGCGTCG	CGCCGGCTC	GATGCGGCTC	TCGATGGGC	4080
AGGGCTCAAC	CGTATCGGGC	GCACGGGGCT	ATTCTGTGTC	GTCGAGCATC	CCAGGGCAGC	4140
TCTGCTGCAG	GAGCGGCTC	GCAGGGCCA	TATTCTCACG	CGCAAGTTG	ACTATGCCCC	4200
GACCTGGCTC	AGGGTCGGTC	TTGCGCCTGA	CGCGGCTGGT	GACCCGACGC	TGGCGGACGC	4260
GCTTGGCCGC	ATGGAGCTCT	GAGGTGTCGG	AGACGATCCT	GCTCATTC	GGCGTGGCGC	4320
TGGTGATCGA	CCCGCTTGTG	GGCGATCCGG	ACTGGCTCTG	GGCGCGCGTG	CCGCATCCGG	4380
TCGTGTTTT	CGGCAAGGGC	ATCGGCTTT	TCGACGCG	GCTGAACCGG	GAGGACCTG	4440
AGGATAGCGC	GCGCAAATT	CGTGGCGTCG	TCGCGATCT	TTTGTGCTT	GGCATCAGCG	4500
CCTGGGTCGG	CATCTGCTG	CATCGCCTGT	TCGCGCTC	CGGACCGCTC	GGCTTCTGC	4560
TCGAGGGCGT	TCTGGTCGCG	GTCTTCTGG	CACAGAACAG	CCTCGCCGAT	CACGTGCGTC	4620
GCCTGGCCGG	GGGCTTGC	CAGGGCGGGC	TGGAAGGGCG	CGTGGCCGCC	GTGTCGATGA	4680
TCGTTGGTCG	CGATCCAAAG	ACGCTCGACG	AGCCGGCGGT	CTGCCGTGCC	GCGATCGAAA	4740
GCCTTGGCGA	GAATTTCTCC	GACGGCGTCG	TGGCGCCGGC	CTTCTGGTAC	GCGGTTGCCG	4800
GCCTGCCGGG	GCTTCTTGC	TACAAGATGC	TGAACACCGC	CGATTGATG	ATCGGCCACA	4860
AGTCGCCGAA	ATATCTGCAC	TTCGGCTGGG	CCTCGGCCG	ACTCGACGAT	CTCGCCAACC	4920
TGCCGGCAGC	GAGGCTCTCG	ATCCTTTGA	TCTCAGCCGG	TGCGCTGATC	CATCGTGGCG	4980
CCAGCGCCGC	CAAGGATGCG	CTGACCGTGG	CCCTTCGCGA	CCATGGCCTG	CACCGCTCGC	5040
CGAACCTCCGG	CTGGCCGGAA	CGGGCCATGG	CCGGCGCGCT	CGATCTGCA	CTTGCCGGTC	5100
CGCGGATCTA	TGGCGCGTC	AAGGTCAGCG	AACCTATGAT	CAACGGTCCG	GGCCGAGCGG	5160
TTGCAACAAG	CGAAGACATC	GACGCCGGTA	TTGCTGTATT	TTATGGCGCC	TGTACGGTCA	5220
TGGCCGGGTT	TGTTCTTGCA	ATCGCAATGA	TTTGTGCG	GAAGTTGACC	TTCGCATTAA	5280
GACTCTGCTT	TCCATATGTA	TTAAGATCGT	ATCATATTG	ATCAGTTATT	CTCCTGGAAC	5340
GTTTGGTTCC	ACCGGTACGT	GTTCGTCTTC	CCGGAGAGAG	AAGCATGCGC	AAAAGCTT	5398

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8753 base pairs  
 (B) TYPE: Nucleic Acid

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(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Pseudomonas denitrificans  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:

(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Nucleotide Sequence of the 5' to 3' strand from the 8753 bp EcoRII fragment of Pseudomonas denitrificans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAATTCTGCCA	GCGCCTACAT	GGCTGACCTC	AAGCAGTTCC	TCGTGGCCCA	GAAGAACGAG	60
GGCCGGCAGA	TTTTCCCTCG	CGGGCCTGAG	TATTTTCGCG	CGCTGACCT	GACGCCGCTC	120
GACAAGGTGC	GCGTGGTCAT	TCTCGGCCAG	GATCCCTATC	ACGGTACGG	CCAGCGGCAT	180
GGGCTCTGCT	TCAGCGTTCG	CCCCGGTGTC	CGGACGCCGC	CGTCGCTGGT	CAACATCTAC	240
AAGGAAGTGA	ATACCGATCT	CGGTATTCCG	CCGGCGCGTC	ACGGTTTTCT	CGAAAGCTGG	300
GCAAGGCAGG	GCGTGTCTGCT	TTTGAACAGC	GTGCTGACGG	TAGAGCGCGG	GAACGTGCGT	360
CACACCAGGG	TCACGGTTGG	GAAAAGTTCA	CGGATGCGAT	CATCCGTGCG	GTCAACGAGG	420
CCGAGCATCC	CGTCGTCTTC	ATGCTTTGGG	GCTCCTATGC	GCAGAAAGAAG	GCGGCCCTCG	480
TCGACCGCTC	GGCCCATCTT	GTCCTGAGGG	CACCACTCC	GTGCGCGCTC	TCAGCCCATT	540
CCGGCTTCT	GGGCTGCCGG	CATTTTCCC	AGGCAATGC	CTTCTCGAA	AGCAAAAGGCT	600
TCGATCCGAT	CGACTGGCGG	CTGCCGGAAA	ATCCGGCTGC	GGACATCAAC	TGAAGGCTTG	660
GCGGAATGA	GGGCTTTGTC	GTGCCCCCTGA	GGTCTTGCT	TGGCGCGGC	GATCCGCCCTA	720
AGACGCCCGA	ACGAAATGGC	GGAGGGGGGC	ATGCGAAAAA	TTCTGATCAT	CGGCATCGGT	780
TCGGGCAATC	CCGAACACAT	GACCGTGCAG	GCGATCAACG	CGCTGAACTG	CGCCGACGTG	840
CTCTTATCC	CGACCAAGGG	AGCGAAGAACG	ACCGAGCTTG	CCGAAGTGC	CCGCGACATC	900
TGCGCCCGCT	ACGTCACCGC	CAAGGACAGC	CGCACCGTC	AGTCGCGGT	GCCCGTGC	960
CGCACCGAAG	GGCTCAGCTA	TGACGGCAGC	GTCGATGACT	GGCACGCCA	GATCGCTGGG	1020
ATTTACGAAG	CGCTTCTATC	GAAGGAGTTG	GGCGAAGAGG	GAACCTGGCGC	GTTCCTCGTC	1080
TGGGGCGACC	CGATGCTCTA	TGACAGCACC	ATTGCGATCG	TCGAGCGGGT	CAAGGCACGC	1140
GGTGAGGTCG	CCTTCGCTA	CGACGTCATT	CCCGGGATCA	CCAGTCTGCA	GGCGCTTGC	1200
GCCAGCCACC	GCATTCCGCT	GAACCTCGTC	GGCAAGCCGG	TGGAGATCAC	CACGGGGCGT	1260
CGGCTGCACG	AAGCTTTCC	CGAGAACAGC	CAGACCTCGG	TCGTCTATGCT	CGATGGCGAA	1320
CAGGCGTTTC	AGCGGGTCTA	GGACCCGGAG	GCGGAGATCT	ATTGGGGCGC	CTATCTCGC	1380
ACGCGGGATG	AGATCGTCAT	TTCCGGCCGC	GTGGCTGAGG	TGAAGGACCG	GATCCTTGAA	1440
ACGCGGGCGG	CGGCGCGCGC	GAAGATGGGA	TGGATCATGG	ACATCTATCT	CCTGCAGCAAG	1500
GGCGCCGACT	TCGACGAGTG	ACGGGGAGGG	CCGATCTGC	TCGTGTTTG	TCTCACTCAA	1560
GGTTTGCCTG	TGTGTTATAG	CGTCTTAAGA	GGCTTCTTA	GGGAGGAGAA	CCTCAAGTGA	1620
TGACGGATT	GATGACCAAGC	TGCGCCCTTC	CATTGACCGG	AGATGCCGCC	ACCGTCGCTT	1680
CGATGCCCG	CGGCGCCTGC	CCGTCCTTGG	CAGAGCCGAT	GCAGACCCGGC	GACGGCCTGC	1740
TCGTGAGGGT	GAGGCCAACG	GATGACAGCC	TGACGCTGCC	GAAGGTCATT	GCCCTTGCCA	1800
CGGCTGCCGA	GCGCTTCGGC	AATGGCATCA	TCGAGATTAC	CGCGCGCGGA	AACCTGCAGC	1860
TTCGCGGCC	GAGCGCGGCT	TCGGTCCAA	GGCTGGCGCA	GGCGATCGGC	GATGCGGAGA	1920
TCGCCATTGC	CGAGGGGGCTC	GCGATCGAGG	TGCCGCCCT	GGCCGGCATC	GACCCGGACG	1980
AGATGCCGA	TCCGCGGCCG	ATTGCCACTG	AGCTTCGTGA	AGCGTTGGAT	GTGCGCCAGG	2040

TGCCGTTGAA	GCTTGACCC	AAATTATCCG	TCGTATCGA	TAGCCGTGGC	CGGTTGGTC	2100
TCGGCGCTGT	CGTCGCCGAC	ATTGCCCTTC	AGGCGGTTTC	GACTGTGCG	GGGGTGGCCT	2160
GGGTGCTGTC	GCTTGGCGC	ACGTCAACGA	AGGCATCGAG	CGTCGGGACG	TTGGCCGGCA	2220
ACGCGGTCGT	GCCGCCCTG	ATCACCAATT	TCGAGAAACT	GGCGAGCCTG	GGCACGACGA	2280
TGCGGGCG	CGATCTGGAC	CCGTCGGAAA	TCCGCGCGCT	CTGTCGCTGT	GAGACATCGT	2340
CCGAACGCC	GGCCGCTCG	CGTCGGCG	CAATACCCGG	CATTATGCG	CTGGGTAACG	2400
CCGACACCGT	TCTCGGCC	GGTCTGGCT	TTGCTCAGGT	GGAGGCGGCC	GCGCTGGCAT	2460
CCTACCTGCA	TCAGGTCCAG	GCGCTTGGCG	CCAATGCGAT	CCGCGTTGCG	CCCGGGCACG	2520
CCTTCTCGT	CCTCGGCC	TGCCCCGAGA	CCGCGGCTGT	GGCGCAGAGC	CTGGCAGCGT	2580
CACACGGTT	TCGCATTGCC	GAGCAGGATC	CGCGCAATGC	GATGCCACC	TGCGCCGGCA	2640
GCAAGGGTTG	CGCCTCGGG	TGGATGGAAA	CCAAGGGCAT	GGCCGAGCGC	CTCGTCGAGA	2700
CGGCGCCGGA	ATTGCTCGAC	GGGTCGCTCA	CCGTGCATCT	CTCCGGCTGC	GCCAAGGGCT	2760
GCGCCGGCC	GAAGCGTCC	GAACTGACGC	TTGTCGGTGC	GCCATCAGGA	TACGGGTTG	2820
TCGTAATGG	GGCTGCCAAT	GGCTTGCCAA	CGCCTACAC	CGATGAGAAT	GAATGGGAT	2880
CCGCCCTTGC	CGGGCTCGGC	CGGCTGGTGC	GGCAAAACAA	AGACGCTGGC	GAATCGGC	2940
AGTCTGTCT	TACACGGCTC	GGAGCTGCGC	GCGTCTCGC	AGCGTTGAA	CAGGGATAGA	3000
CATGCTGAG	TATGATTACA	TTCGCGATGG	CAACGCCATC	TACGAGCGTT	CCTTCGCCAT	3060
CATCCGCGCC	GAGGCCGATC	TGTCGCGCTT	CTCCGAAGAG	GAAGCGGATC	TGGCTGTGCG	3120
CATGGTGCAC	GCCTGCGGTT	CCGTCGAGGC	GACCAGGCAG	TTCGTGTGTTT	CTCCCGATTT	3180
CGTAAGCTG	GGCCGTCGG	CGCTGAAAGC	CGGTGCGCCG	ATCCTCTGCG	ATGCCGAGAT	3240
GGTTGCGCAC	GGTGTCAACCC	GCGCCCGTCT	GCCGGCCGGC	AACGAGGTGA	TCTGCACGCT	3300
GCGCGATCCT	CGCACGCCG	CACTTGCGGC	CGAGATCGGC	AACACCCGCT	CCGGCGCAGC	3360
CCTGAAGCTC	TGGAGCGAGC	GGCTGGCCGG	TTCGGTGGTC	GCGATCGGC	ACGCGCCGAC	3420
GGCGTTGTT	TTCTCTTGG	AAATGCTGCG	CGACGGCGCG	CCGAAGCCGG	CGGCAATCCT	3480
CGGCATGCC	GTCGGTTTCG	TCGGTGC	GGAATCGAAG	GATGCGCTGG	CCGAGAACTC	3540
CTATGGCGTT	CCCTTCGCA	TCGTGCGCGG	CCGCCTCGG	GGGAGTGCCA	TGACGGCGGC	3600
AGCGCTTAAC	TCGCTCGCA	GGCCGGGCT	GTGAGCGGC	TCGGCGTGGG	GCGCTGATC	3660
GGTGTGGGA	CGGGCCCCGG	TGATCCGGAA	CTTTTGACGG	TCAAGGCGGT	GAAGGCGCTC	3720
GGGCAAGCCG	ATGTGCTTGC	CTATTCGCC	AAGGCCGGC	GAAGCGGTAA	CGGCGCGCG	3780
GTGGTCGAGG	GTCTGCTGAA	GCCCAGTCTT	GTCGAGCTC	CGCTATACTA	TCCGGTGACG	3840
ACCGAAATCG	ACAAGGACGA	TGGGCC	AAGACCCAGA	TCACCGACTT	CTACAATGCG	3900
TCGGCCGAAG	CGGTAGCGC	GCATTTGCC	GCCGGGCGCA	CGGTGCGCGT	GCTCAGTGAA	3960
GGCAGCCCGC	TGTTCTATGG	TTCC	CATCTGCGAT	TGCGGCTCGC	CAATCGTTT	4020
CCGGTCGAGG	TGATCCCCGG	CATTACCGCC	ATGTCGGCT	GTTGGTGC	TGCCGGCCTG	4080
CCGCTGTG	AGGGCGACGA	CGTGCCTCG	GTGCTTC	GCACCATGGC	CGAGGCCGAG	4140
CTCGGCCGCA	GGCTTGC	TACCGAAGCC	GCCGTGATCA	TGAAGGTC	GCGCAATTG	4200
CCGAAGATCC	GTCGGGCGCT	CGCTGCC	GGCGT	ACCAGGCCGT	CTATGTCGAA	4260
CGCGGACGA	TGAAGAACGC	GCGCATGACG	GCTTTGCGG	AAAAGGCCG	CGACGAGGC	4320
CCCTATTCT	CGCTGGTGC	CGTCCC	TGGAAGGACC	GACCATGACC	GGTACGCTCT	4380
ATGTCGTCG	TACCGGACCG	GGCAGCGCA	AGCAGATGAC	GCCGGAAACG	GCGGAAGCCG	4440
TTGCGCCG	TCAGGAGTTT	TACGGCTACT	TTCCCTATCT	CGACCGGCTG	AACCTCAGAC	4500
CGGATCAGAT	CCGTGTCGCC	TCGGAC	GCGAGGAGCT	CGATCGGGCA	CAGGTCGCG	4560
TGACGCGGGC	TGCGGCAGGC	GTGAAGGTC	GCATGGTCTC	CGGTGGCGAT	CCCGGTGTCT	4620
TTGCCATGGC	GGCCGCCG	TGCGAGGCGA	TCGACAAGGG	ACCGGCGAA	TGGAAGTCG	4680
TTGAACTGGT	GATCACGCC	GGCGT	CGATGTC	CGTTGCC	CGCATCGCG	4740
CGCCGCTCG	TCATGATTTC	TGTGC	CGCTTCCG	CAATCTGAA	CCCTGGGAAG	4800
TCATCACCCG	GGGTCTCAGG	CTGGCG	AAGCGGCTT	CGTCATTGCC	CTCTACAA	4860
CGATCAGCAA	GGCGCGGCC	TGGCAGCTC	GTGAGGCTT	CGAGCTTCTG	CGCAGCGTTC	4920
TGCCGGAAG	CGTTCCG	ATCTTCCG	GTGCG	GCGCCGGAC	GAACGGATCG	4980
CGGTGATGCC	GCTCGCGAG	GCCGATGCC	ACCGCGCGA	CATGGCGACC	TGCGTCATCA	5040
TCGGCTCGCC	GGAGACGCGC	ATCGTCGAGC	GCGACGCCA	ACCCGATCTC	GTCTACACAC	5100
CGCGCTTCTA	TGCAGGGCG	AGCCAGTGA	CGATGCGTT	GAGTGCCTG	TGCAACTGC	5160
CGACCGTCG	CACGTCGCG	GGCTTGC	GCTCGACCAT	GATCACCTG	ATGCCGAGCC	5220
GGCGCGCTG	GGCAATCTTG	CCGTAGGTG	CGCTGCCACC	GCTGTTCTG	GCGACGATCA	5280
CATCGATCTG	CCGACTCCTG	AGCAACGCGG	CTTCGTC	TTCCGAAAG	GGACCGGTG	5340
CCAGGATCGC	CTCC	GGCAGATTAA	GGCGCGGCGT	CACCGGATCG	ACGCTGCCG	5400
TGACGTAGCT	GTGCTGCG	GCGACCTCGA	AGTGGAAAGC	TTCTGTCGA	CCTATGCCA	5460
GGAAAGACCG	GGCGT	TCACCGAGCG	CGCTGACGGC	CTCGACAAACG	CTATGACAG	5520
CAGTCCAGCG	GTCGCCAGGC	AGGGCACCC	ATTCGGTGC	GCGGAGGGCG	ATAAGCGAA	5580
CGCCGGTTCT	TTGCGT	TCCGCGCGT	TGTGCAAAT	GCGTGC	AAGGGGTGCG	5640
TCGCATCGAC	CAGCAGCG	ATGTTTCTG	CATGCA	ATGCGCCAGC	CCATCCGCG	5700
CGCCAAAGCC	GCCGATGCGC	GTCTGACCG	GCTGCGGCC	CGGGTCCG	GTGCGGCCGG	5760
CCAGCGAGAT	GGCGGTGTC	TAGCGACAT	CTTCGGCAA	GCGCGCGCG	AGTTCGCGT	5820

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CCTCGGTGGT	GCCACCCAGA	ATCAGAATAC	GAGGTTTTC	CATGGCTGAC	GTGTCGAACA	5880
CGAACCACGC	CATAGTCTCC	CCCTGGCTGA	CCGTATCGG	TATCGGTGAG	GATGGTGTAG	5940
CGGGTCTCGG	CGACGAGGCC	AAGCGGCTGA	TCGCCGAAGC	GCCGGTCGTC	TACGGCGGCC	6000
ATCGTCATCT	GGAGCTCGCC	GCCTCCCTCA	TCACCGGCGA	AGGCCACAAT	TGGCTAAGCC	6060
CCCTCGAACG	CTCGGTCGTC	GAGATCGTCG	CGCGTCGCGG	CAGCCCCGTG	GTGGTGCCTG	6120
CCTCGGGCGA	CCCCTTCTTC	TTCGCGCTCG	GCCTGACGCT	GCGCGCCGC	ATCGCCTCGG	6180
CCGAAATACG	CACGCTTCG	GCGCGCTCGT	CGATCAGTCT	TGCCGCCTCG	CGCCTCGGCT	6240
GGGCCTGCA	GGATGCGACG	CTCGTCTCCG	TACATGGGCG	GCCGCTGGAT	CTGGTGGGAC	6300
CGCATTGCA	TCCGGGGGCG	CGTGTGCTTA	CGCTCACGTC	GGACGGTGC	GGTCCCGGAG	6360
ACCTTGCAGA	GCTTCTGGTT	TCAAGCGGCT	TCGGTCAGTC	GCGACTGACC	GTGCTCGAAG	6420
CGCTGGCGG	CGCCGGCGAA	CGGGTGACGA	CGCAGATCGC	CGCGCGCTTC	ATGCTCGGCC	6480
TCGTGCATCC	TTTGAACGTC	TGCGCCATTG	AGGTGGCGGC	CGACGAGGGC	GCGCGCATCC	6540
TGCCGCTTGC	CGCCGGCCGC	GACGATGCGC	TGTTCGAAC	TGACGGGCAG	ATCACCAAGC	6600
GCGAGGTGCG	GGCGCTGACG	CTGTCGGCAC	TCGCACCGCG	CAAGGGCGAA	CTGCTATGGG	6660
ACATCGGCGG	CGGCTCCGGC	TCGATCGGC	TCGAATGGAT	GCTCGCCGAT	CCGACCATGC	6720
AGGCATCAC	CATCGAGGTT	GAGCGGAGC	GGGCAGCGCG	CATCGGCCGC	AACGCGACGA	6780
TGTTGGCGT	GCCCGGGCTG	ACGGTTGTCG	AAGGCAGGGC	GCCGGCGGCCG	CTTGGCGGCC	6840
TGCCACAACC	GGACGCGATC	TTCATCGGCG	CGGGCGGAG	CGAACAGCGC	GTCAATGAAAG	6900
CAGCGATCGA	GGCGCTCAAG	TCAGGCGGAC	GGCTGGTTC	CAACGCGGTG	ACGACGGACA	6960
TGGAAGCGGT	GCTGCTCGAT	CATCACCGC	GGCTCGGGG	TTCGCTGATC	CGCATCGATA	7020
TCGCCTGTC	AGGACCCATC	GGCAGCATGA	CCGGCTGAA	GCCGGCCATG	CCGGTCAACC	7080
AATGGTCGTG	GACGAAGGGC	TAAAGCAGTT	CCAGCGAAAG	TGTGACGGCG	TTTTGCGTCC	7140
GGAACTGCGC	AAGAAAAAAGA	AAGAGTAACC	TATGACGTA	CATTTCATCG	GCGCCGGCCC	7200
GGGAGCCGCA	GACCTGATCA	CGGGTGTG	TCGCACCTG	ATCGGGCGCT	GCCCGGTCTG	7260
CCTTACGCC	GGCTCGATCG	TCTCGCCGGA	GCTGCTGCGA	TATTGCCCCG	CGGGCGCCCG	7320
CATTGTCGAT	ACGGCGCCGA	TGTCCCTCGA	CGAGATCGAG	GCGGAGTATG	TGAAGGCCGA	7380
AGCCGAAGGG	CTCGACGTGG	CGCGGCTTCA	TCAGGGCGAC	CTTTGGTCT	GGAGTGTGT	7440
GGCCGAACAG	ATCCGCGGGC	TCGAGAAC	TGGCATCGCC	TATACGATGA	CGCCGGCGT	7500
TCCTTCCTT	GGGGCGGCCG	CTTCAGCGCT	CGGTGCGAA	TTGACCATTC	CGGCCGTGGC	7560
CCAGAGCCTG	GTGCTGACCC	CGCTTTCGGG	CCGCGCCTCG	CCGATGCCGA	ACTCAGAAC	7620
GCTTTCGCT	TTCGGCGCTA	CGGGATCGAC	GCTGGCAATC	CACCTTGC	TCCATGCGCT	7680
TCAGCAGGTG	GTCGAGGAAC	TGACGCCGCT	CTACGGTGC	GACTGCCCG	TCGCCATCGT	7740
CGTCAAGGCC	TCCCTGGCCG	ACGAACGCGT	GGTGCAGCGC	ACGCTCGGTG	ACATGCCGC	7800
CAAGGTGGCG	GAAGAGCCGA	TCGAGCGCAC	GGCGCTGATC	TTCGTCGGTC	CGGGGCTCGA	7860
AGCCTCCGAT	TTCCGTGAAA	GTCGCTCTA	CGATCCCGCC	TATCAGCGC	GCTTCAGAGG	7920
GCGCGGCCGA	TAGGCCGAC	TCCCTCGGGG	GTCGGCTTAA	GTTTCCCCT	GAGAGGGTTT	7980
TGAAACCTAT	TCTGCGGGT	CTTCAGCGCG	CGGCGCTGC	TTGAGCGGA	CGCCGCGCTT	8040
TTCTCGACG	CGGTGCGCGT	AGAGCGCTGC	CTGTCGAAGC	AGCATCAGCG	TCACCAGCGT	8100
GGTGGCGACG	ACGAAGACGA	TGATCAGGAT	TTCTGGAAT	ACCCAGCGGC	TCTGCAGCAC	8160
GGCAAAGCAG	ATGATAGAGG	CGGCGCAGAT	CATCAGTACG	CCGCGCGCTGG	TCGCCAGCGT	8220
CGGTGCGTGC	AGGCCTCGT	AGAAAGCTGT	GAACCGGAGC	AAGCCGACGG	AGCCGATCAG	8280
CGCCACTGCG	GCGCCGAGGA	CGGTGAGCCC	CGACGACGAGA	ACGGCTGCC	AGACGGAAG	8340
GTCGGTGAGG	TGGCTCATTC	GATGATCTCC	CCGCGCATCA	GGAACATTGCC	GAAGGGGATC	8400
GACGAGACGA	AGCCGATCAA	AGCCACGATC	AGGGCGGACT	CGAAATAGAG	CGAGTTGCC	8460
GTGCGGATGC	CGAAGGTCAA	GAGCATCAGC	ATGGCGTTGA	TATAGAGCGT	GTGAGGCCG	8520
AGGATACGGT	CCTGGGCGCG	CGGTCCCCCTC	ACCATGCGAT	AGAAGGCAA	AGCCATCGCC	8580
AGGCCGAGCA	TGATCTGGGC	AATCAGGATC	GACCAGATGA	TTGAAAGTTC	CATCATCCGA	8640
ATATTCCTT	CAGGGCGGTC	TCATAGCGCT	TGACCGTATC	GAGCCAGATG	TCCTCGTTCT	8700
CCATGTCGAG	CACGTGGAAG	AGCAGGGACT	TGCGGCCGCG	ATCCGGGGAA	TTC	8753

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 843 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:

10724598

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: *coba*
- (B) LOCATION: 1141-1980 bp of SEQ ID NO: 1
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGATCGACG	ACCTCTTGC	CGGATTGCCG	GCGCTCGAAA	AAGGTTCGGT	CTGGCTGGTC	60
GGCGCCGGCC	CCGGCGATCC	CGGCCCTGTTG	ACGCTGCATG	CGGCCAATGC	GCTGCGCCAG	120
GCGGATGTGA	TCGTGCATGA	TGCGCTGGTC	AACGAGGATT	GCCTGAAGCT	CGCGCGGCCG	180
GGCGCCGTGC	TGGAGTTGTC	GGGCAAGCGT	GGCGGCAAGC	CGTCGCCGAA	GCAGCGCGAC	240
ATCTCGCTTC	GCCTCGTCGA	ACTCGCGC	GCCGGCAACC	GGGTGCTGCG	CCTCAAAGGC	300
GGCGATCCCT	TCGTCTTCGG	TCGCGGTGGC	GAGGAGGCGC	TGACGCTGGT	CGAACACCAAG	360
GTGCCGTTCC	GAATCGTGCC	CGGCATCACC	GCCGGTATCG	GCAGGGCTTGC	CTATGCCGGC	420
ATTCCCGTGA	CCCATCGCGA	GGTCAACACC	GCGGTCACTT	TCCTGACTGG	CCATGATTCC	480
TCCGGGCTGG	TGCCGGATCG	CATCAACTGG	CAGGGCATCG	CCAGCGGCTC	GCCTGTCATC	540
GTCATGTACA	TGGCGATGAA	ACATATCGGC	GCGATCACCG	CCAACCTCAT	TGCCGGCGGC	600
CGCTCGCCGG	ACGAACCGGT	CGCCTTCGTC	TGCAACGCCG	CGACGCCGCA	GCAGGCCGTG	660
CTGGAAACGA	CGCTTGCAGCG	TGCAGAGGCC	GATGTTGCAG	CGGCAGGGCT	GGAGCCGCCG	720
GCGATCGTCG	TCGTCGGCAG	GGTGGTGCAG	CTGCGCGCAG	CGCTCGACTG	GATCGGCCGC	780
CTGGACGGGC	GCAAGCTTGC	CGCCGACCCCG	TTCGCCAATC	GCATTCTCAG	GAACCCGGCA	840
TGA						843

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBA
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ile Asp Asp Leu Phe Ala Gly Leu Pro Ala Leu Glu Lys Gly Ser  
 1 5 10 15  
 Val Trp Leu Val Gly Ala Gly Pro Gly Asp Pro Gly Leu Leu Thr Leu  
 20 25 30  
 His Ala Ala Asn Ala Leu Arg Gln Ala Asp Val Ile Val His Asp Ala  
 35 40 45  
 Leu Val Asn Glu Asp Cys Leu Lys Leu Ala Arg Pro Gly Ala Val Leu  
 50 55 60  
 Glu Phe Ala Gly Lys Arg Gly Gly Lys Pro Ser Pro Lys Gln Arg Asp  
 65 70 75 80  
 Ile Ser Leu Arg Leu Val Glu Leu Ala Arg Ala Gly Asn Arg Val Leu  
 85 90 95  
 Arg Leu Lys Gly Gly Asp Pro Phe Val Phe Gly Arg Gly Gly Glu Glu  
 100 105 110  
 Ala Leu Thr Leu Val Glu His Gln Val Pro Phe Arg Ile Val Pro Gly  
 115 120 125  
 Ile Thr Ala Gly Ile Gly Gly Leu Ala Tyr Ala Gly Ile Pro Val Thr  
 130 135 140  
 His Arg Glu Val Asn His Ala Val Thr Phe Leu Thr Gly His Asp Ser  
 145 150 155 160  
 Ser Gly Leu Val Pro Asp Arg Ile Asn Trp Gln Gly Ile Ala Ser Gly  
 165 170 175  
 Ser Pro Val Ile Val Met Tyr Met Ala Met Lys His Ile Gly Ala Ile  
 180 185 190  
 Thr Ala Asn Leu Ile Ala Gly Gly Arg Ser Pro Asp Glu Pro Val Ala  
 195 200 205  
 Phe Val Cys Asn Ala Ala Thr Pro Gln Gln Ala Val Leu Glu Thr Thr  
 210 215 220  
 Leu Ala Arg Ala Glu Ala Asp Val Ala Ala Gly Leu Glu Pro Pro  
 225 230 235 240  
 Ala Ile Val Val Val Gly Glu Val Val Arg Leu Arg Ala Ala Leu Asp  
 245 250 255  
 Trp Ile Gly Ala Leu Asp Gly Arg Lys Leu Ala Ala Asp Pro Phe Ala  
 260 265 270  
 Asn Arg Ile Leu Arg Asn Pro Ala  
 275 280

## (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:

10724598

(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: cobb  
(B) LOCATION: 1980-3283 bp of SEQ ID NO: 1  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGAGCGGAT	TGCTGATTGC	CGCACCCGCG	TCCGGCTCCG	GCAAGACGAC	GGTGACGCTC	60
GGGCTGATGC	GCGCCCTGAA	GAGGCGCGC	GTGGCGATCG	CGCCCGGCAA	GGCGGGGCCG	120
GAATATATCG	ATCCCCTT	CCACCGGGCA	GCGACCGCG	AGCCCTGCTT	CAACTACGAC	180
CCCTGGCGA	TGCGCCCCGA	ACTGCTGCTT	GCCAATGCGT	CGCATGTGGC	CTCCGGCGGG	240
CGCACATTGA	TCGTCGAGGC	GATGATGGGA	CTGCATGACG	GTGCTGCCGA	CGGCTCGGGA	300
ACGCCAGCGG	ACCTCGCCG	GACGCTGAAC	CTTGCGGTCA	TTCTGGTGGT	CGATTGCGCC	360
CGCATGTC	AGTCGGTGC	CGCCCTCGT	CGCGGCTATG	CGGATCATCG	CGACGATATC	420
CGGGTGGTTG	GGCTCATCCT	CAACAAGGCT	GGCAGCGATC	GGCATGAAAT	GATGCTGCGC	480
GATGCGCTCG	GCAAGGTGCG	CATGCCCTGC	TTCCGGCTGC	TCCGGCAGGA	CAGCGCATTG	540
CAACTGCCG	AGCGCCATCT	CGGGCTCGT	CAGGCAGGGCG	AACACTCAGC	GCTTGAGGGC	600
TTCATCGAGG	CGGCGGCCG	CGGGGTGAG	GCTGCCCTGC	ATCTCGACGC	CATCCGCCCTG	660
ATCGCGACGA	TTTTCCCGCA	GGTGCCCGCG	GGCGCCGATG	CCGAGCGTTT	GCGGCCGCTC	720
GGTCAGCGCA	TCGCGGTGCG	GCGCGATATC	GCCTTTCGCT	TCTGCTACGA	GCACCTGCTT	780
TACGGCTGGC	GGCAAGGCGG	CGCGGAGATT	TCCTTCTTCT	CGCCGCTCGC	CGACGAGGGG	840
CCGGATGCGG	CAGCGATGC	CGTCTATCTT	CCGGGGGGTT	ATCCGGAGCT	GCATGCGGGG	900
CAGCTGAGCG	CCGCCGCCG	ATTCCGTTCC	GGCATGCATT	CCGCGGCCGA	ACGCGGCCGC	960
CGCATCTTCG	GGAGTGCGG	CGGCTATATG	GTGCTCGCG	AAGGGCTTGT	CGCTGCCGAT	1020
GGCACACGCT	ACGACATGCT	CGGCCCTGCT	CGCCTCGTA	CCAGTTTGC	CGAGCGCAGG	1080
CGGCACCTCG	GCTATCGCCG	CGTCTGCGCT	GTCGACAACG	CCTTCTTCGA	TGGACCCATG	1140
ACGGCGACG	AATTCCACTA	TGCGACCATC	GTCGCCGAAG	GGGCAGGCCGA	TCGGCTGTTT	1200
GCGGTAGCG	ACGCCGCCG	CGAGGATCTC	GGCCAGGGCG	GCCTCCGGCG	CGGCCCTGTC	1260
GCGGGTTCT	TCATGCATCT	GATGACGTC	GCAGGTGCTG	CATGA		1305

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 434 amino acids  
(B) TYPE: Amino Acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: Pseudomonas denitrificans  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: COBB  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Translation product of SEQ ID NO:5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10724598

Met Ser Gly Leu Leu Ile Ala Ala Pro Ala Ser Gly Ser Gly Lys Thr  
1 5 10 15  
Thr Val Thr Leu Gly Leu Met Arg Ala Leu Lys Arg Arg Gly Val Ala  
20 25 30  
Ile Ala Pro Gly Lys Ala Gly Pro Asp Tyr Ile Asp Pro Ala Phe His  
35 40 45  
Ala Ala Ala Thr Gly Glu Pro Cys Phe Asn Tyr Asp Pro Trp Ala Met  
50 55 60  
Arg Pro Glu Leu Leu Leu Ala Asn Ala Ser His Val Ala Ser Gly Gly  
65 70 75 80  
Arg Thr Leu Ile Val Glu Ala Met Met Gly Leu His Asp Gly Ala Ala  
85 90 95  
Asp Gly Ser Gly Thr Pro Ala Asp Leu Ala Ala Thr Leu Asn Leu Ala  
100 105 110  
Val Ile Leu Val Val Asp Cys Ala Arg Met Ser Gln Ser Val Ala Ala  
115 120 125  
Leu Val Arg Gly Tyr Ala Asp His Arg Asp Asp Ile Arg Val Val Gly  
130 135 140  
Val Ile Leu Asn Lys Val Gly Ser Asp Arg His Glu Met Met Leu Arg  
145 150 155 160  
Asp Ala Leu Gly Lys Val Arg Met Pro Val Phe Gly Val Leu Arg Gln  
165 170 175  
Asp Ser Ala Leu Gln Leu Pro Glu Arg His Leu Gly Leu Val Gln Ala  
180 185 190  
Gly Glu His Ser Ala Leu Glu Gly Phe Ile Glu Ala Ala Ala Ala Arg  
195 200 205  
Val Glu Ala Ala Cys Asp Leu Asp Ala Ile Arg Leu Ile Ala Thr Ile  
210 215 220  
Phe Pro Gln Val Pro Ala Ala Ala Asp Ala Glu Arg Leu Arg Pro Leu  
225 230 235 240  
Gly Gln Arg Ile Ala Val Ala Arg Asp Ile Ala Phe Ala Phe Cys Tyr  
245 250 255  
Glu His Leu Leu Tyr Gly Trp Arg Gln Gly Gly Ala Glu Ile Ser Phe  
260 265 270  
Phe Ser Pro Leu Ala Asp Glu Gly Pro Asp Ala Ala Ala Asp Ala Val  
275 280 285  
Tyr Leu Pro Gly Gly Tyr Pro Glu Leu His Ala Gly Gln Leu Ser Ala  
290 295 300  
Ala Ala Arg Phe Arg Ser Gly Met His Ser Ala Ala Glu Arg Gly Ala  
305 310 315 320  
Arg Ile Phe Gly Glu Cys Gly Gly Tyr Met Val Leu Gly Glu Gly Leu  
325 330 335  
Val Ala Ala Asp Gly Thr Arg Tyr Asp Met Leu Gly Leu Leu Pro Leu  
340 345 350  
Val Thr Ser Phe Ala Glu Arg Arg Arg His Leu Gly Tyr Arg Arg Val  
355 360 365  
Val Pro Val Asp Asn Ala Phe Phe Asp Gly Pro Met Thr Ala His Glu  
370 375 380  
Phe His Tyr Ala Thr Ile Val Ala Glu Gly Ala Ala Asp Arg Leu Phe  
385 390 395 400  
Ala Val Ser Asp Ala Ala Gly Glu Asp Leu Gly Gln Ala Gly Leu Arg  
405 410 415  
Arg Gly Pro Val Ala Gly Ser Phe Met His Leu Ile Asp Val Ala Gly  
420 425 430  
Ala Ala

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1002 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: *cobC*
- (B) LOCATION: 3281-4279 bp of SEQ ID NO: 1
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGAGCGCAC	CGATCGTTCA	TGGTGGCGGC	ATCACCGAGG	CCGAGCGCG	CTATGGCGGC	60
CGGCCTGAAG	ACTGGCTCGA	TCTGTCGACC	GGCATCAATC	CATGCCCGT	CGCCTTGC	120
GCGGTCCTG	AGCGCGCCTG	GCACCGGCTG	CCGGATCGGC	AGACGGTAGA	TGATGCGCGG	180
AGCGCCGCCG	CCGACTACTA	CCGCACCAAC	GGCGTGTG	CTTTGCCGGT	GCCGGGCACC	240
CAGTCGGTGA	TCCAGCTCCT	GCCACGTCTT	GCTCCGGCCA	ACAGGCACGT	CGCGATTTTC	300
GGGCCGACCT	ATGGCGAGTA	TGCCCGCGTG	CTTGAAGCGG	CCGGCTTGC	TGTCGATCGC	360
GTCGCGGATG	CCGACGCGCT	CACGCCGAA	CATGGGCTTG	TCATCGTCGT	CAACCCCAAC	420
AACCCGACCG	GCCGCGCCTT	GGC GCCGGCG	GAGCTTCTGG	CGATCGCCGC	AAGGCAGAAG	480
GCGAGCGCGC	GACTGCTGCT	GGTGTGATGAG	GCCTTCGGCG	ATCTTGAGCC	GCAACTGAGT	540
GTCGCTGGTC	ACCGCGTCAGG	GCAAGGCAAC	CTCATCGTCT	TCCGCTCCTT	CGGCAAGTTC	600
TTCGGGCTTG	CGGGCCTGCG	CCTCGGCTTC	GTCGTTGCGA	CCGAGCCAGT	GCTTGATCC	660
TTTGCGGATT	GGCTCGGTTG	CTGGGCTGTC	TCCGGCCCGG	CGTTGACGAT	CTCGAAAGCG	720
CTGATGCGAGG	GCGATACGAA	GGCGATCGCG	CGGGGCATCC	TCGAGCGTCG	CGCCGGCCTC	780
GATGCGGCTC	TCGATGGGGC	AGGGCTAAC	CGTATCGGC	GCACGGGGCT	ATTCGTGCTG	840
GTCGAGCATC	CCAGGGCAGC	TCTGCTGAG	GAGCGGCTCT	GCGAGGCCCA	TATTCTCACG	900
CGCAAGTTCG	ACTATGCC	GACCTGGCTC	AGGGTCGTC	TTGCGCCTGA	CGCGGCTGGT	960
GACCGACGGC	TGGCGGACGC	GCTTGGCCGC	ATGGAGCTCT	GA		1002

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:

10724598

(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: COBC  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Translation product of SEQ ID NO:7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ser Ala Pro Ile Val His Gly Gly Gly Ile Thr Glu Ala Ala Ala  
1 5 10 15  
Arg Tyr Gly Gly Arg Pro Glu Asp Trp Leu Asp Leu Ser Thr Gly Ile  
20 25 30  
Asn Pro Cys Pro Val Ala Leu Pro Ala Val Pro Glu Arg Ala Trp His  
35 40 45  
Arg Leu Pro Asp Arg Gln Thr Val Asp Asp Ala Arg Ser Ala Ala Ala  
50 55 60  
Asp Tyr Tyr Arg Thr Asn Gly Val Leu Pro Leu Pro Val Pro Gly Thr  
65 70 75 80  
Gln Ser Val Ile Gln Leu Leu Pro Arg Leu Ala Pro Ala Asn Arg His  
85 90 95  
Val Ala Ile Phe Gly Pro Thr Tyr Gly Glu Tyr Ala Arg Val Leu Glu  
100 105 110  
Ala Ala Gly Phe Ala Val Asp Arg Val Ala Asp Ala Asp Ala Leu Thr  
115 120 125  
Ala Glu His Gly Leu Val Ile Val Val Asn Pro Asn Asn Pro Thr Gly  
130 135 140  
Arg Ala Leu Ala Pro Ala Glu Leu Leu Ala Ile Ala Ala Arg Gln Lys  
145 150 155 160  
Ala Ser Gly Gly Leu Leu Val Asp Glu Ala Phe Gly Asp Leu Glu  
165 170 175  
Pro Gln Leu Ser Val Ala Gly His Ala Ser Gly Gln Gly Asn Leu Ile  
180 185 190  
Val Phe Arg Ser Phe Gly Lys Phe Phe Gly Leu Ala Gly Leu Arg Leu  
195 200 205  
Gly Phe Val Val Ala Thr Glu Pro Val Leu Ala Ser Phe Ala Asp Trp  
210 215 220  
Leu Gly Pro Trp Ala Val Ser Gly Pro Ala Leu Thr Ile Ser Lys Ala  
225 230 235 240  
Leu Met Gln Gly Asp Thr Lys Ala Ile Ala Ala Gly Ile Leu Glu Arg  
245 250 255  
Arg Ala Gly Leu Asp Ala Ala Leu Asp Gly Ala Gly Leu Asn Arg Ile  
260 265 270  
Gly Gly Thr Gly Leu Phe Val Leu Val Glu His Pro Arg Ala Ala Leu  
275 280 285  
Leu Gln Glu Arg Leu Cys Glu Ala His Ile Leu Thr Arg Lys Phe Asp  
290 295 300  
Tyr Ala Pro Thr Trp Leu Arg Val Gly Leu Ala Pro Asp Ala Ala Gly  
305 310 315 320  
Asp Arg Arg Leu Ala Asp Ala Leu Ala Arg Met Glu Leu  
325 330

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 972 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

10724598

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: *Pseudomonas denitrificans*  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: cobb  
(B) LOCATION: 4284-5252 bp of SEQ ID NO: 1  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GTGTCGGAGA	CGATCCTGCT	CATTCTCGCG	CTGGCGCTGG	TGATCGACCG	CGTTGTCGGC	60
GATCCGGACT	GGCTCTGGGC	GCGCGTCCG	CATCCGGTCG	TGTTTTTCGG	CAAGGCCATC	120
GGCTTTTCG	ACGCGCGGCT	GAACCGGGAG	GACCTCGAGG	ATAGCGCGCG	CAAATTCGT	180
GGCGTCGTCG	CGATCCTTTT	GTTGCTTGGC	ATCAGCGCCT	GGTTCGGCCA	TCTGCTGCAT	240
CGCCTGTCG	CCGTCCTCGG	ACCGCTCGC	TTTCTGCTCG	AGGCGGTTCT	GGTCGCGGTC	300
TTCCTGGCAC	AGAAGAGCCT	CGCCGATCAC	GTGCGTCGCG	TGGCCGGGGG	CTTGCACAG	360
GGCGGGCTGG	AAGGCAGGGCG	TGCCGCCGTG	TCGATGATCG	TTGGTCGCGA	TCCAAAGACG	420
CTCGACGAGC	CGGCGGTCTG	CCGTGCGCGC	ATCGAAAGCC	TTGCCGAGAA	TTTCTCCGAC	480
GGCGTCGTCG	CGCCGGCCCT	CTGGTACCGC	GTTGCCGCC	TGCCGGGGCT	TCTTGCTTAC	540
AAGATGCTGA	ACACCGCCGA	TTCGATGATC	GGCCACAAGT	CGCCGAAATA	TCTGCACCTTC	600
GGCTGGGCCT	CGGCCCCACT	CGACGATCTC	GCCAACCTGC	CGGCAGCGAG	GCTCTCGATC	660
CTTTTGTACT	CAGCGGGTGC	GCTGATCCAT	CGTGGCGCCA	GCGCCGCCAA	GGATGCGCTG	720
ACCGTGGCCC	TTCGCGACCA	TGGCCTGCAC	CGCTCGCCGA	ACTCCGGCTG	GCCGGAAGCG	780
GCCATGGCCG	GCGCGCTCGA	TCTGCAGCTT	GCCGGTCGCG	GGATCTATGG	CGGCGTCAAG	840
GTCAGCGAAC	CTATGATCAA	CGGTCGGGGC	CGAGCGGTTG	CAACAAGCGA	AGACATCGAC	900
GCCGGTATTG	CTGTATTTA	TGGCGCCTGT	ACGGTCATGG	CCGGGTTTGT	TCTTGCAATC	960
GCAATGATTG	GA					972

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 amino acids  
(B) TYPE: Amino Acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: *Pseudomonas denitrificans*  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:

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(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: COBD  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Translation product of SEQ ID NO:9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ser Glu Thr Ile Leu Leu Ile Leu Ala Leu Ala Leu Val Ile Asp  
1 5 10 15  
Arg Val Val Gly Asp Pro Asp Trp Leu Trp Ala Arg Val Pro His Pro  
20 25 30  
Val Val Phe Phe Gly Lys Ala Ile Gly Phe Phe Asp Ala Arg Leu Asn  
35 40 45  
Arg Glu Asp Leu Glu Asp Ser Ala Arg Lys Phe Arg Gly Val Val Ala  
50 55 60  
Ile Leu Leu Leu Gly Ile Ser Ala Trp Phe Gly His Leu Leu His  
65 70 75 80  
Arg Leu Phe Ala Val Leu Gly Pro Leu Gly Phe Leu Leu Glu Ala Val  
85 90 95  
Leu Val Ala Val Phe Leu Ala Gln Lys Ser Leu Ala Asp His Val Arg  
100 105 110  
Arg Val Ala Gly Gly Leu Arg Gln Gly Gly Leu Glu Gly Gly Arg Ala  
115 120 125  
Ala Val Ser Met Ile Val Gly Arg Asp Pro Lys Thr Leu Asp Glu Pro  
130 135 140  
Ala Val Cys Arg Ala Ala Ile Glu Ser Leu Ala Glu Asn Phe Ser Asp  
145 150 155 160  
Gly Val Val Ala Pro Ala Phe Trp Tyr Ala Val Ala Gly Leu Pro Gly  
165 170 175  
Leu Leu Ala Tyr Lys Met Leu Asn Thr Ala Asp Ser Met Ile Gly His  
180 185 190  
Lys Ser Pro Lys Tyr Leu His Phe Gly Trp Ala Ser Ala Arg Leu Asp  
195 200 205  
Asp Leu Ala Asn Leu Pro Ala Ala Arg Leu Ser Ile Leu Leu Ile Ser  
210 215 220  
Ala Gly Ala Leu Ile His Arg Gly Ala Ser Ala Ala Lys Asp Ala Leu  
225 230 235 240  
Thr Val Ala Leu Arg Asp His Gly Leu His Arg Ser Pro Asn Ser Gly  
245 250 255  
Trp Pro Glu Ala Ala Met Ala Gly Ala Leu Asp Leu Gln Leu Ala Gly  
260 265 270  
Pro Arg Ile Tyr Gly Gly Val Lys Val Ser Glu Pro Met Ile Asn Gly  
275 280 285  
Pro Gly Arg Ala Val Ala Thr Ser Glu Asp Ile Asp Ala Gly Ile Ala  
290 295 300  
Val Phe Tyr Gly Ala Cys Thr Val Met Ala Gly Phe Val Leu Ala Ile  
305 310 315 320  
Ala Met Ile

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 465 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: *Pseudomonas denitrificans*  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: *cobe*  
(B) LOCATION: 549-1011 bp of SEQ ID NO: 1  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGCCATCGG	GCCAAACACTC	TGCACAGACG	ACGAAAGCAG	GAGCCGGGCT	GGTGCTCGGG	60
CTCGGCTGCG	AGCGTCGAC	GCCGGCCGAA	GAGGTGATCG	CCCTTGCCTGA	GCGTGCCTT	120
GCCGATGCCG	GTGTTGCGCC	CGGCGATCTG	CGGCTGGTCG	CCTCGCTCGA	TGCTCGGCC	180
GAGGAGCCGG	CGATCCTGGC	GGCCGCTCAG	CATTTCCGCG	TTCCGGCCGC	GTTCTACGAT	240
GCCGCCACGC	TCGAAGCCGA	AGCTTCCCAG	CTCGCCAACC	CGTCCGAGAT	CGTCTTTGCC	300
TACACGGGTT	GTCATGGCGT	TGCCGAGGGT	GCAGCGCTCG	TCGGCGCCGG	TCGCGAAGCC	360
GTGCTGATTG	TGCAGAAAGAT	CGTCTCCGCC	CATGCGACGG	CCGCACTTGC	CGGGCCGGCG	420
ACCTTGCAGCG	CCGAAAAGCG	CATCCAGGCG	CGGGAGGCTG	TCTGA		465

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 amino acids  
(B) TYPE: Amino Acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: *Pseudomonas denitrificans*  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: COBE  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Translation product of SEQ ID NO:11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Pro Ser Gly Gln His Ser Ala Gln Thr Thr Lys Ala Gly Ala Gly  
1 5 10 15  
Leu Val Leu Gly Leu Gly Cys Glu Arg Arg Thr Pro Ala Glu Glu Val  
20 25 30  
Ile Ala Leu Ala Glu Arg Ala Leu Ala Asp Ala Gly Val Ala Pro Gly  
35 40 45  
Asp Leu Arg Leu Val Ala Ser Leu Asp Ala Arg Ala Glu Glu Pro Ala  
50 55 60  
Ile Leu Ala Ala Ala Gln His Phe Ala Val Pro Ala Ala Phe Tyr Asp  
65 70 75 80  
Ala Ala Thr Leu Glu Ala Glu Ala Ser Arg Leu Ala Asn Pro Ser Glu  
85 90 95  
Ile Val Phe Ala Tyr Thr Gly Cys His Gly Val Ala Glu Gly Ala Ala  
100 105 110  
Leu Val Gly Ala Gly Arg Glu Ala Val Leu Ile Val Gln Lys Ile Val  
115 120 125  
Ser Ala His Ala Thr Ala Ala Leu Ala Gly Pro Ala Thr Leu Arg Ala  
130 135 140  
Glu Lys Arg Ile Gln Ala Ala Glu Ala Val  
145 150

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: *cobF*
- (B) LOCATION: 736-1521 bp of SEQ ID NO: 2
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATGGCGGAGG	CGGGCATGCG	CAAATTCTG	ATCATCGCA	TCGGTTCGGG	CAATCCGAA	60
CACATGACCG	TGCAGGCGAT	CAACCGCTG	AACTGCGCCG	ACGTGCTCTT	TATCCCGACC	120
AAGGGAGCGA	AGAAGACCGA	GCTTGCCGAA	GTGCGCCCG	ACATCTGCGC	CCGCTACGTC	180
ACGCGCAAGG	ACAGCCGAC	CGTCGAGTTC	GCGGTGCCG	TGCGGCGCAC	CGAAGGCCTC	240
AGCTATGACG	GCAGCGTCGA	TGACTGGCAC	GCCCAGATCG	CTGGGATTTA	CGAAGCGCTT	300
CTATCGAAGG	AGTTGGCGA	AGAGGGAAC	GGCGCGTTTC	TCGTCTGGGG	CGACCCGATG	360
CTCTATGACA	GCACCATTG	CATCGTCGAG	CGGGTCAAGG	CACCGCGTGA	GGTCGCCCTTC	420

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GCCTACGACG	TCATTCCCGG	GATCACCAGT	CTGCAGGCCG	TTTGCGCCAG	CCACCGCATT	480
CCGCTGAACC	TCGTCGGCAA	GCCGGTGGAG	ATCACCAACGG	GGCGTCGGCT	GCACGAAAGC	540
TTTCCCGAGA	AGAGCCAGAC	CTCGGTGTC	ATGCTCGATG	GCGAACAGGC	GTTTCAGCGG	600
GTCGAGGACC	CGGAGGCGGA	GATCTATTGG	GGCGCCTATC	TCGGCACGCG	GGATGAGATC	660
GTCATTCCG	GCCGCGTGGC	TGAGGTGAAG	GACCGGATCC	TTGAAACGCG	GGCGGCGCG	720
CGCGCGAAGA	TGGGATGGAT	CATGGACATC	TATCTCCTGC	GCAAGGGCGC	CGACTTCGAC	780
GAGTGA						786

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 261 amino acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas denitrificans*
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: COBF
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Translation product of SEQ ID NO:13
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ala Glu Ala Gly Met Arg Lys Ile Leu Ile Ile Gly Ile Gly Ser  
1 5 10 15  
Gly Asn Pro Glu His Met Thr Val Gln Ala Ile Asn Ala Leu Asn Cys  
20 25 30  
Ala Asp Val Leu Phe Ile Pro Thr Lys Gly Ala Lys Lys Thr Glu Leu  
35 40 45  
Ala Glu Val Arg Arg Asp Ile Cys Ala Arg Tyr Val Thr Arg Lys Asp  
50 55 60  
Ser Arg Thr Val Glu Phe Ala Val Pro Val Arg Arg Thr Glu Gly Val  
65 70 75 80  
Ser Tyr Asp Gly Ser Val Asp Asp Trp His Ala Gln Ile Ala Gly Ile  
85 90 95  
Tyr Glu Ala Leu Leu Ser Lys Glu Leu Gly Glu Glu Gly Thr Gly Ala  
100 105 110  
Phe Leu Val Trp Gly Asp Pro Met Leu Tyr Asp Ser Thr Ile Arg Ile  
115 120 125  
Val Glu Arg Val Lys Ala Arg Gly Glu Val Ala Phe Ala Tyr Asp Val  
130 135 140  
Ile Pro Gly Ile Thr Ser Leu Gln Ala Leu Cys Ala Ser His Arg Ile  
145 150 155 160  
Pro Leu Asn Leu Val Gly Lys Pro Val Glu Ile Thr Thr Gly Arg Arg  
165 170 175  
Leu His Glu Ser Phe Pro Glu Lys Ser Gln Thr Ser Val Val Met Leu

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180	185	190
Asp	Gly	Glu
Gly	Gln	Ala
195	190	195
Ala	Phe	Gln
Tyr	Trp	Arg
200	200	205
Gly	Gly	Val
210	215	220
Ala	Ala	Tyr
225	230	235
Arg	Val	Leu
240	245	250
Ala	Ala	Glu
Arg	Lys	Asp
Ala	Met	Gly
255	255	255
Ala	Trp	Ile
Ala	Ile	Asp
Asp	Met	Ile
260	250	250
Glu	Tyr	Tyr

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1380 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas denitrificans*
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: *cobG*
  - (B) LOCATION: 1620-2999 bp of SEQ ID NO: 2
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGACGGATT	TGATGACCAG	CTGCGCCCTT	CCATTGACCG	GAGATGCCGG	CACCGTCGCT	60
TCGATGCGCC	GCGGCGCCTG	CCCGTCCTTG	GCAGAGCCGA	TGCAGACCGG	CGACGGCCTG	120
CTCGTGGGG	TGAGGCCAAC	GGATGACAGC	CTGACGCTGC	CGAAGGTCAT	TGCCCTTGCC	180
ACGGCTGCCG	AGCGCTTCGG	CAATGGCATC	ATCGAGATTA	CCGCGCGCGG	AAACCTGCAG	240
CTTCGCGGCC	TGAGCGCGGC	TTCGGTGCCA	AGGCTGGCGC	AGGCGATCGG	CGATGCGGAG	300
ATCGCCATTG	CCGAGGGGCT	CGCGATCGAG	GTGCCGCC	TGGCCGGCAT	CGACCCGGAC	360
GAGATCGCCG	ATCCGCGGCC	GATTGCCACT	GAGCTTCGTG	AAGCGTTGGA	TGTGCGCCAG	420
GTGCGCTTGA	AGCTTGACCC	CAAATTATCC	GTCGTCATCG	ATAGCGGTGG	CCGGTTTGGT	480
CTCGGCGCTG	TCGTCGCCGA	CATTGCGCTT	CAGGCGGTTT	CGACTGTCGC	GGGGGTGGCC	540
TGGGTGCTGT	CGCTTGGCGG	CACGTCAACG	AAGGCATCGA	CGCTCGGGAC	GTTGGCCGGC	600
AACGGCGTCG	TGCCGGCCCT	GATCACCATT	CTCGAGAAC	TGGCGAGCCT	GGGCACCGACG	660
ATGCGCGGGC	GCGATCTGGA	CCCGTCGGAA	ATCCGCGCGC	TCTGTCGCTG	TGAGACATCG	720
TCCGAACGCC	CGGCCGCTCC	CGCTTCGGCC	GCAATACCCG	GCATTATGCG	GCTGGGTAAC	780
GCCGACACCG	TTCTCGGCCT	CGGCTCTGGCC	TTTGCTCAGG	TGGAGGCCGC	CGCGCTGGCA	840
TCCTACCTGC	ATCAGGTCCA	GGCGCTTGCG	GCCAATGCGA	TCCGGCTTGC	GCCCAGGCAC	900
GCCTTCTTCG	TCCTCGGCCT	TTGCCCGAG	ACCGCGGCTG	TGGCGCAGAG	CCTGGCAGCG	960
TCACACGGTT	TTCGCATTGC	CGAGCAGGAT	CCGCGCAATG	CGATGCGCAC	CTGCGCCGGC	1020
AGCAAGGGTT	GCGCCTCGGC	GTGGATGGAA	ACCAAGGGCA	TGGCCGAGCG	CCTCGTCGAG	1080

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ACGGCGCCGG	AATTGCTCGA	CGGGTGCCTC	ACCGTGCATC	TCTCCGGCTG	CGCCAAGGGC	1140
TGCGCCCGGC	CGAAGCCGTC	CGAACTGACG	CTTGTGCGTG	CGCCATCAGG	ATACGGGCTT	1200
GTCGTAATG	GGGCTGCCAA	TGGCTTGCCA	AGCGCCTACA	CCGATGAGAA	TGGAATGGGA	1260
TCCGCCCTTG	CCCGGCTCGG	CCGGCTGGTG	CGGAAACACA	AAGACGCTGG	CGAATCGGCG	1320
CAGTCTGTC	TTACACGGCT	CGGAGCTGCG	CGCGTCTCGG	CAGCGTTCGA	ACAGGGATAG	1380

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 459 amino acids  
(B) TYPE: Amino Acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: *Pseudomonas denitrificans*  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: COBG  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Translation product of SEQ ID NO:15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Thr Asp Leu Met Thr Ser Cys Ala Leu Pro Leu Thr Gly Asp Ala  
1 5 10 15  
Gly Thr Val Ala Ser Met Arg Arg Gly Ala Cys Pro Ser Leu Ala Glu  
20 25 30  
Pro Met Gln Thr Gly Asp Gly Leu Leu Val Arg Val Arg Pro Thr Asp  
35 40 45  
Asp Ser Leu Thr Leu Pro Lys Val Ile Ala Leu Ala Thr Ala Ala Glu  
50 55 60  
Arg Phe Gly Asn Gly Ile Ile Glu Ile Thr Ala Arg Gly Asn Leu Gln  
65 70 75 80  
  
Leu Arg Gly Leu Ser Ala Ala Ser Val Pro Arg Leu Ala Gln Ala Ile  
85 90 95  
Gly Asp Ala Glu Ile Ala Ile Ala Glu Gly Leu Ala Ile Glu Val Pro  
100 105 110  
Pro Leu Ala Gly Ile Asp Pro Asp Glu Ile Ala Asp Pro Arg Pro Ile  
115 120 125  
Ala Thr Glu Leu Arg Glu Ala Leu Asp Val Arg Gln Val Pro Leu Lys  
130 135 140  
Leu Ala Pro Lys Leu Ser Val Val Ile Asp Ser Gly Gly Arg Phe Gly  
145 150 155 160  
Leu Gly Ala Val Val Ala Asp Ile Arg Leu Gln Ala Val Ser Thr Val  
165 170 175  
Ala Gly Val Ala Trp Val Leu Ser Leu Gly Gly Thr Ser Thr Lys Ala  
180 185 190  
Ser Ser Val Gly Thr Leu Ala Gly Asn Ala Val Val Pro Ala Leu Ile

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195                   200                   205  
Thr Ile Leu Glu Lys Leu Ala Ser Leu Gly Thr Thr Met Arg Gly Arg  
210                   215                   220  
Asp Leu Asp Pro Ser Glu Ile Arg Ala Leu Cys Arg Cys Glu Thr Ser  
225                   230                   235                   240  
Ser Glu Arg Pro Ala Ala Pro Arg Ser Ala Ala Ile Pro Gly Ile His  
245                   250                   255  
Ala Leu Gly Asn Ala Asp Thr Val Leu Gly Leu Gly Leu Ala Phe Ala  
260                   265                   270  
Gln Val Glu Ala Ala Ala Leu Ala Ser Tyr Leu His Gln Val Gln Ala  
275                   280                   285  
Leu Gly Ala Asn Ala Ile Arg Leu Ala Pro Gly His Ala Phe Phe Val  
290                   295                   300  
Leu Gly Leu Cys Pro Glu Thr Ala Ala Val Ala Gln Ser Leu Ala Ala  
305                   310                   315                   320  
Ser His Gly Phe Arg Ile Ala Glu Gln Asp Pro Arg Asn Ala Ile Ala  
325                   330                   335  
Thr Cys Ala Gly Ser Lys Gly Cys Ala Ser Ala Trp Met Glu Thr Lys  
340                   345                   350  
Gly Met Ala Glu Arg Leu Val Glu Thr Ala Pro Glu Leu Leu Asp Gly  
355                   360                   365  
Ser Leu Thr Val His Leu Ser Gly Cys Ala Lys Gly Cys Ala Arg Pro  
370                   375                   380  
Lys Pro Ser Glu Leu Thr Leu Val Gly Ala Pro Ser Gly Tyr Gly Leu  
385                   390                   395                   400  
Val Val Asn Gly Ala Ala Asn Gly Leu Pro Ser Ala Tyr Thr Asp Glu  
405                   410                   415  
Asn Gly Met Gly Ser Ala Leu Ala Arg Leu Gly Arg Leu Val Arg Gln  
420                   425                   430  
Asn Lys Asp Ala Gly Glu Ser Ala Gln Ser Cys Leu Thr Arg Leu Gly  
435                   440                   445  
Ala Ala Arg Val Ser Ala Ala Phe Glu Gln Gly  
450                   455

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 633 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: Pseudomonas denitrificans  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: cobH  
(B) LOCATION: 3002-3634 bp of SEQ ID NO: 2  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGCCTGAGT	ATGATTACAT	TCGCGATGGC	AACGCCATCT	ACGAGCGTTC	CTTCGCCATC	60
ATCCGCGCCG	AGGCCGATCT	GTCGCGCTTC	TCCGAAGAGG	AAGCGGATCT	GGCTGTGCGC	120
ATGGTGCACG	CCTGCGGTT	CGTCGAGGCG	ACCAGGCAGT	TCGTGTTTC	TCCCGATTTC	180
GTAAGCTCGG	CCCCTGCGGC	GCTGAAAGCC	GGTGCGCCGA	TCCTCTGCGA	TGCCGAGATG	240
GTTGCGCACG	GTGTCACCCG	CGCCCGTCTG	CCGGCCGGCA	ACGAGGTTGAT	CTGCACGCTG	300
CGCGATCCTC	GCACGCCCGC	ACTTGCAGGC	GAGATCGGCA	ACACCCGCTC	CGCCGAGGCC	360
CTGAAGCTCT	GGAGCGAGCG	GCTGGCCGGT	TCGGTGGTCG	CGATCGGCAA	CGCGCCGACG	420
GCGTTGTTCT	TCCTCTTGGA	AATGCTGCGC	GACGGCGCGC	CGAAGCCGGC	GGCAATCCTC	480
GGCATGCCCG	TCGGTTTCGT	CGGTGCGGGCG	GAATCGAAGG	ATGCCTGGC	CGAGAACTCC	540
TATGGCGTTC	CCTTCGCCAT	CGTGCAGGCC	CGCCTCGCGC	GGAGTGCAT	GACGGCGGCA	600
GCGTTAACT	CGCTCGCGAG	GCCGGGCGT	TGA			633

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBH
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Pro	Glu	Tyr	Asp	Tyr	Ile	Arg	Asp	Gly	Asn	Ala	Ile	Tyr	Glu	Arg	
1		5				10								15		
Ser	Phe	Ala	Ile	Ile	Arg	Ala	Glu	Ala	Asp	Leu	Ser	Arg	Phe	Ser	Glu	
							20			25				30		
Glu	Glu	Ala	Asp	Leu	Ala	Val	Arg	Met	Val	His	Ala	Cys	Gly	Ser	Val	
							35			40			45			
Glu	Ala	Thr	Arg	Gln	Phe	Val	Phe	Ser	Pro	Asp	Phe	Val	Ser	Ser	Ala	
							50			55			60			
Arg	Ala	Ala	Leu	Lys	Ala	Gly	Ala	Pro	Ile	Leu	Cys	Asp	Ala	Glu	Met	
							65			70			75		80	
Val	Ala	His	Gly	Val	Thr	Arg	Ala	Arg	Leu	Pro	Ala	Gly	Asn	Glu	Val	
							85			90			95			
Ile	Cys	Thr	Leu	Arg	Asp	Pro	Arg	Thr	Pro	Ala	Leu	Ala	Glu	Ile		
							100			105			110			
Gly	Asn	Thr	Arg	Ser	Ala	Ala	Leu	Lys	Leu	Trp	Ser	Glu	Arg	Leu		
							115			120			125			
Ala	Gly	Ser	Val	Val	Ala	Ile	Gly	Asn	Ala	Pro	Thr	Ala	Leu	Phe	Phe	

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130	135	140													
Leu	Leu	Glu	Met	Leu	Arg	Asp	Gly	Ala	Pro	Lys	Pro	Ala	Ala	Ile	Leu
145				150						155					160
Gly	Met	Pro	Val	Gly	Phe	Val	Gly	Ala	Ala	Glu	Ser	Lys	Asp	Ala	Leu
										165	170				175
Ala	Glu	Asn	Ser	Tyr	Gly	Val	Pro	Phe	Ala	Ile	Val	Arg	Gly	Arg	Leu
										180	185				190
Gly	Gly	Ser	Ala	Met	Thr	Ala	Ala	Leu	Asn	Ser	Leu	Ala	Arg	Pro	
										195	200				205
Gly	Leu														
															210

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 738 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: Pseudomonas denitrificans
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: cobi
  - (B) LOCATION: 3631-4368 bp of SEQ ID NO: 2
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	60					
TGTAGCGGCG	TGGCGCTGGG	GCGCTGTATC	GGTGTGGGA	CCGGCCCCGG	TGATCCGGAA	120
CTTTTGACGG	TCAAGGCGGT	GAAGGCGCTC	GGGCAAGCCG	ATGTGCTTGC	CTATTTGCC	180
AAGGCCGGGC	GAAGCGGTAA	CGGCCGCGCG	GTGGTCGAGG	GTCTGCTGAA	GCCCGATCTT	240
GTCGAGCTGC	CGCTATACTA	TCCGGTGACG	ACCGAAATCG	ACAAGGACGA	TGGGCCCTAC	300
AAGACCCAGA	TCACCGACTT	CTACAATGCG	TCGGCCGAAG	CGGTAGCGGC	GCATCTTGCC	360
GCCGGGCGCA	CGGTCGCGGT	GCTCACTGAA	GGCGACCCGC	TGTTCTATGG	TTCCTACATG	420
CATCTGCATG	TGCGGCTCGC	CAATCGTTTC	CCGGTCGAGG	TGATCCCCGG	CATTACCGCC	480
ATGTCCGGCT	GTTGGTCGCT	TGCCGGCTCTG	CCGCTGGTGC	AGGGCGACGA	CGTGCTCTCG	540
GTGCTTCCGG	GCACCATGGC	CGAGGCCGAG	CTCGGCCGA	GGCTTGCAGA	TACCGAACCC	600
GCCGTTGATCA	TGAAGGTCGG	GCGCAATTG	CCGAAGATCC	GTCTGGCGCT	CGCTGCCTCC	660
GGCCGCTCTCG	ACCAGGCCGT	CTATGTCGAA	CGCGGCACGA	TGAAGAACGC	GGCGATGACG	720
GCTCTTGCAG	AAAAGGCCGA	CGACGAGGCG	CCCTATTTCT	CGCTGGTGC	CGTTCCCGGC	738
TGGAAGGACCG	GACCATGAA					

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 245 amino acids
  - (B) TYPE: Amino Acid

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(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Pseudomonas denitrificans  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:

(A) NAME/KEY: COBI  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Translation product of SEQ ID NO:19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Ser Gly Val Gly Val Gly Arg Leu Ile Gly Val Gly Thr Gly Pro  
1 5 10 15  
Gly Asp Pro Glu Leu Leu Thr Val Lys Ala Val Lys Ala Leu Gly Gln  
20 25 30  
Ala Asp Val Leu Ala Tyr Phe Ala Lys Ala Gly Arg Ser Gly Asn Gly  
35 40 45  
Arg Ala Val Val Glu Gly Leu Leu Lys Pro Asp Leu Val Glu Leu Pro  
50 55 60  
Leu Tyr Tyr Pro Val Thr Thr Glu Ile Asp Lys Asp Asp Gly Ala Tyr  
65 70 75 80  
Lys Thr Gln Ile Thr Asp Phe Tyr Asn Ala Ser Ala Glu Ala Val Ala  
85 90 95  
Ala His Leu Ala Ala Gly Arg Thr Val Ala Val Leu Ser Glu Gly Asp  
100 105 110  
Pro Leu Phe Tyr Gly Ser Tyr Met His Leu His Val Arg Leu Ala Asn  
115 120 125  
Arg Phe Pro Val Glu Val Ile Pro Gly Ile Thr Ala Met Ser Gly Cys  
130 135 140  
Trp Ser Leu Ala Gly Leu Pro Leu Val Gln Gly Asp Asp Val Leu Ser  
145 150 155 160  
Val Leu Pro Gly Thr Met Ala Glu Ala Glu Leu Gly Arg Arg Leu Ala  
165 170 175  
Asp Thr Glu Ala Ala Val Ile Met Lys Val Gly Arg Asn Leu Pro Lys  
180 185 190  
Ile Arg Arg Ala Leu Ala Ala Ser Gly Arg Leu Asp Gln Ala Val Tyr  
195 200 205  
Val Glu Arg Gly Thr Met Lys Asn Ala Ala Met Thr Ala Leu Ala Glu  
210 215 220  
Lys Ala Asp Asp Glu Ala Pro Tyr Phe Ser Leu Val Leu Val Pro Gly  
225 230 235 240  
Trp Lys Asp Arg Pro  
245

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 764 base pairs

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- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas denitrificans*
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: *cobj*
  - (B) LOCATION: 4365-5129 bp of SEQ ID NO: 2
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATGACCGGTA	CGCTCTATGT	CGTCGGTACC	GGACCGGGCA	GCGCCAAGCA	GATGACGCCG	60
GAAACGGCGG	AAGCCGTTGC	GGCCGCTCAG	GAGTTTTACG	GCTACTTTCC	CTATCTCGAC	120
CGGCTGAACC	TCAGACCGGA	TCAGATCCGT	GTCGCCCTCGG	ACAACCGCGA	GGAGCTCGAT	180
CGGGCACAGG	TCGCGCTGAC	GCAGGGCTGCG	GCAGGCGTGA	AGGTCTGCAT	GGTCTCCGGT	240
GGCGATCCCG	GTTGCTTTGC	CATGGCGGCC	GCCGTCCTGCG	AGGCAGATCGA	CAAGGGACCG	300
GCGGAATGGA	AGTCGGTTGA	ACTGGTGTAC	ACGCCCGGCG	TGACCGCGAT	GCTGCCCGTT	360
GCCGCCCGCA	TCGGCGCGCC	GCTCGGTCAT	GATTTCTGTG	CGATCTCGCT	TTCCGACAAT	420
CTGAAGCCCT	GGGAAGTCAT	CACCCGGCGT	CTCAGGCTGG	CGGGCGGAAGC	GGGCTTCGTC	480
ATTGCCCTCT	ACAATCCGAT	CAGCAAGGCG	CGGCCCTGGC	AGCTCGGTGA	GGCCTTCGAG	540
CTTCTGCGCA	GCGTTCTGCC	GGCAAGCGTT	CCGGTCATCT	TCGGCCGTGC	GGCCGGCGG	600
CCGGACGAAC	GGATCGCGGT	GATGCCGCTC	GGCGAGGGCCG	ATGCCAACCG	CGCCGACATG	660
GCGACCTGCG	TCATCATCGG	CTCGCCGGAG	ACGCGCATCG	TCGAGCGCGA	CGGCCAACCC	720
GATCTCGTCT	ACACACCGCG	CTTCTATGCA	GGGGCGAGCC	AGTG		764

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 254 base pairs
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas denitrificans*
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:

(ix) FEATURE:  
 (A) NAME/KEY: COBJ  
 (B) LOCATION:  
 (C) IDENTIFICATION METHOD:  
 (D) OTHER INFORMATION: Translation product of SEQ ID NO:21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Thr Gly Thr Leu Tyr Val Val Gly Thr Gly Pro Gly Ser Ala Lys  
 1 5 10 15  
 Gln Met Thr Pro Glu Thr Ala Glu Ala Val Ala Ala Ala Gln Glu Phe  
 20 25 30  
 Tyr Gly Tyr Phe Pro Tyr Leu Asp Arg Leu Asn Leu Arg Pro Asp Gln  
 35 40 45  
 Ile Arg Val Ala Ser Asp Asn Arg Glu Glu Leu Asp Arg Ala Gln Val  
 50 55 60  
 Ala Leu Thr Arg Ala Ala Ala Gly Val Lys Val Cys Met Val Ser Gly  
 65 70 75 80  
 Gly Asp Pro Gly Val Phe Ala Met Ala Ala Val Cys Glu Ala Ile  
 85 90 95  
 Asp Lys Gly Pro Ala Glu Trp Lys Ser Val Glu Leu Val Ile Thr Pro  
 100 105 110  
 Gly Val Thr Ala Met Leu Ala Val Ala Ala Arg Ile Gly Ala Pro Leu  
 115 120 125  
 Gly His Asp Phe Cys Ala Ile Ser Leu Ser Asp Asn Leu Lys Pro Trp  
 130 135 140  
 Glu Val Ile Thr Arg Arg Leu Arg Leu Ala Ala Glu Ala Gly Phe Val  
 145 150 155 160  
 Ile Ala Leu Tyr Asn Pro Ile Ser Lys Ala Arg Pro Trp Gln Leu Gly  
 165 170 175  
 Glu Ala Phe Glu Leu Leu Arg Ser Val Leu Pro Ala Ser Val Pro Val  
 180 185 190  
 Ile Phe Gly Arg Ala Ala Gly Arg Pro Asp Glu Arg Ile Ala Val Met  
 195 200 205  
 Pro Leu Gly Glu Ala Asp Ala Asn Arg Ala Asp Met Ala Thr Cys Val  
 210 215 220  
 Ile Ile Gly Ser Pro Glu Thr Arg Ile Val Glu Arg Asp Gly Gln Pro  
 225 230 235 240  
 Asp Leu Val Tyr Thr Pro Arg Phe Tyr Ala Gly Ala Ser Gln  
 245 250

## (2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 786 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ORIGINAL SOURCE:  
 (A) ORGANISM: Pseudomonas denitrificans  
 (B) STRAIN:  
 (C) INDIVIDUAL ISOLATE:  
 (D) DEVELOPMENTAL STAGE:  
 (E) HAPLOTYPE:  
 (F) TISSUE TYPE:  
 (G) CELL TYPE:  
 (H) CELL LINE:

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(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: cobK  
(B) LOCATION: compl. strand of 2861-3634 bp of SEQ ID NO:2  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATGGCGGGTT	CGCTGTTCGA	CACGTCA GCC	ATGGAAAAAC	CTCGTATTCT	GATTCTGGGT	60
GGCACCAACG	AGGCACGCGA	ACTCGCGCGC	CGCTTGGCCG	AAGATGTCCG	CTACGACACC	120
GCCATCTCGC	TGGCCGGCCG	CACCGCGGAC	CGCGGGCCGC	AGCCGGTCAA	GACGCGCATC	180
GGCGGCTTG	GCGGCGCCG	TGGGCTGGCG	CATTTCTGTC	ATGACAAAAA	CATCGCGCTG	240
CTGGTCGATG	CGACGCACCC	CTTTGCGCA	CGCATTTCGC	ACAACGCCGC	GGACGCAGCG	300
CAAAGAACCG	GCGTTGCGCT	TATCGCCCTC	CGCCGACCGG	AATGGGTGCC	CCTGCCTGGC	360
GACCGCTGGA	CTGCTGTCGA	TAGCGTTGTC	GAGGCCGTCA	GCGCGCTCGG	TGATCGGCAG	420
CGCCGCGTCT	TCTGGCGAT	AGGTCGACAG	GAAGCTTTCC	ACTTCGAGGT	CGCGCCGCAG	480
CACAGCTACG	TCATCGCGAG	CGTCGATCCG	GTGACGCCGC	CGCTTAATCT	GCCCAGCCAG	540
GAGGCCATCC	TGGCGACCCGG	TCCCTTTGCG	GAAGCCGACG	AAGCCGCGTT	GCTCAGGAGT	600
CGGCAGATCG	ATGTGATCGT	CGCCAAGAAC	AGCGGTGGCA	GCGCCACCTA	CGGCAAGATT	660
GCGCAGCGC	GCCGGCTCGG	CATCGAGGTG	ATCATGGTCG	AGCGGCGCAA	GCCCCGCGGAC	720
GTGCCGACGG	TGGCAGTTG	CGACGAGGCA	CTCAACCGCA	TCGCTCACTG	GCTCGCCCCCT	780
						786

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 amino acids  
(B) TYPE: Amino Acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: Pseudomonas denitrificans  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: COBK  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Translation product of SEQ ID NO:23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ala Gly Ser Leu Phe Asp Thr Ser Ala Met Glu Lys Pro Arg Ile  
1 5 10 15  
Leu Ile Leu Gly Gly Thr Thr Glu Ala Arg Glu Leu Ala Arg Arg Leu  
20 25 30  
Ala Glu Asp Val Arg Tyr Asp Thr Ala Ile Ser Leu Ala Gly Arg Thr  
35 40 45

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Ala Asp Pro Arg Pro Gln Pro Val Lys Thr Arg Ile Gly Gly Phe Gly  
50 55 60  
Gly Ala Asp Gly Leu Ala His Phe Val His Asp Glu Asn Ile Ala Leu  
65 70 75 80  
Leu Val Asp Ala Thr His Pro Phe Ala Ala Arg Ile Ser His Asn Ala  
85 90 95  
Ala Asp Ala Ala Gln Arg Thr Gly Val Ala Leu Ile Ala Leu Arg Arg  
100 105 110  
Pro Glu Trp Val Pro Leu Pro Gly Asp Arg Trp Thr Ala Val Asp Ser  
115 120 125  
Val Val Glu Ala Val Ser Ala Leu Gly Asp Arg Arg Arg Arg Val Phe  
130 135 140  
Leu Ala Ile Gly Arg Gln Glu Ala Phe His Phe Glu Val Ala Pro Gln  
145 150 155 160  
His Ser Tyr Val Ile Arg Ser Val Asp Pro Val Thr Pro Pro Leu Asn  
165 170 175  
Leu Pro Asp Gln Glu Ala Ile Leu Ala Thr Gly Pro Phe Ala Glu Ala  
180 185 190  
Asp Glu Ala Ala Leu Leu Arg Ser Arg Gln Ile Asp Val Ile Val Ala  
195 200 205  
Lys Asn Ser Gly Gly Ser Ala Thr Tyr Gly Lys Ile Ala Ala Ala Arg  
210 215 220  
Arg Leu Gly Ile Glu Val Ile Met Val Glu Arg Arg Lys Pro Ala Asp  
225 230 235 240  
Val Pro Thr Val Gly Ser Cys Asp Glu Ala Leu Asn Arg Ile Ala His  
245 250 255  
Trp Leu Ala Pro Ala  
260

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1242 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
(A) ORGANISM: *Pseudomonas denitrificans*  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY: *cobL*  
(B) LOCATION: 5862-7103 bp of SEQ ID NO: 2  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATGGCTGACG	TGTCGAACAG	CGAACCCGCC	ATAGTCTCCC	CCTGGCTGAC	CGTCATCGGT	60
ATCGGTGAGG	ATGGTGTAGC	GGGTCTCGGC	GACGAGGCCA	AGCGGCTGAT	CGCCGAAGCG	120
CCGGTCGTCT	ACGGCGGCCA	TCGTCATCTG	GAGCTCGCCG	CCTCCCTCAT	CACCGCGAA	180
GCGCACAAATT	GGCTAAGCCC	CCTCGAACGC	TCGGTCGTG	AGATCGTCGC	GCGTCGCGGC	240
AGCCCGGTGG	TGGTGCTTGC	CTCGGGCGAC	CCGTTCTTCT	TCGGCGTCGG	CGTGACGCTG	300
GCGCGCCGCA	TCGCCTCGGC	CGAAATACGC	ACGCTTCCGG	CGCCGTCGTC	GATCAGTCTT	360
GCCGCCTCGC	GCCTCGGCTG	GGCGCTGCAG	GATGCACGC	TCGTCTCCGT	ACATGGCGG	420
CCGCTGGATC	TGGTGCGACC	GCATTGAT	CCGGGGGGCGC	GTGTGTTAC	GCTCACGTCG	480
GACGGTGCAGG	GTCCCGAGA	CCTTGCAG	CTTCTGGTTT	CAAGCGGCTT	CGGTCACTCG	540
CGACTGACCG	TGCTCGAACG	GCTGGCGGC	GCCGGCGAAC	GGGTGACGAC	GCAGATCGCC	600
GCGCGCTTCA	TGCTCGGCCT	CGTGATCCT	TTAACGTCT	GCGCCATTGA	GGTGGCGGCC	660
GACGAGGGCG	CGCGCATCCT	GCCGCTGCC	GCCGGCCGCG	ACGATGCGCT	GTTCGAACAT	720
GACGGGCAGA	TCACCAAGCG	CGAGGTGCGG	GCGCTGACGC	TGTCGGCACT	CGCACCGCGC	780
AAGGGCGAAC	TGCTATGGGA	CATCGCGGC	GGCTCCGGCT	CGATCGGCAT	CGAATGGATG	840
CTCGCGATC	CGACCATGCA	GGCGATCACC	ATCGAGGTTG	AGCCGGAGCG	GGCAGCGCGC	900
ATCGGGCGCA	ACGCGACGAT	GTTCCGGCGT	CCCAGGCTGA	CGGTTGTCGA	AGGCAGGGCG	960
CCGGCCGGCG	TTGCCGGCCT	GCCACAACCG	GACCGATCT	TCATCGGGCG	CGGCGGCCAGC	1020
GAAGACGGCG	TCATGGAAGC	AGCGATCGAG	GCGCTCAAGT	CAGGCGGACG	GCTGGTTGCC	1080
AACCGGGTGA	CGACGGACAT	GGAAGCGGTG	CTGCTCGATC	ATCACGCGCG	GCTGGCGGT	1140
TCGCTGATCC	GCATCGATAT	CGCGCGTGCA	GGACCCATCG	GCGGCATGAC	CGGCTGGAAG	1200
CCGGCCATGC	CGGTACCCCA	ATGGTCGTGG	ACGAAGGGCT	AA		1242

## (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 413 amino acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas denitrificans*
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: COBL
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Translation product of SEQ ID NO:25
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Asp Val Ser Asn Ser Glu Pro Ala Ile Val Ser Pro Trp Leu  
 1 5 10 15  
 Thr Val Ile Gly Ile Gly Glu Asp Gly Val Ala Gly Leu Gly Asp Glu  
 20 25 30  
 Ala Lys Arg Leu Ile Ala Glu Ala Pro Val Val Tyr Gly Gly His Arg  
 35 40 45  
 His Leu Glu Leu Ala Ala Ser Leu Ile Thr Gly Glu Ala His Asn Trp  
 50 55 60

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Leu Ser Pro Leu Glu Arg Ser Val Val Glu Ile Val Ala Arg Arg Gly  
 65 70 75 80  
 Ser Pro Val Val Val Leu Ala Ser Gly Asp Pro Phe Phe Phe Gly Val  
 85 90 95  
 Gly Val Thr Leu Ala Arg Arg Ile Ala Ser Ala Glu Ile Arg Thr Leu  
 100 105 110  
 Pro Ala Pro Ser Ser Ile Ser Leu Ala Ala Ser Arg Leu Gly Trp Ala  
 115 120 125  
 Leu Gln Asp Ala Thr Leu Val Ser Val His Gly Arg Pro Leu Asp Leu  
 130 135 140  
 Val Arg Pro His Leu His Pro Gly Ala Arg Val Leu Thr Leu Thr Ser  
 145 150 155 160  
 Asp Gly Ala Gly Pro Arg Asp Leu Ala Glu Leu Leu Val Ser Ser Gly  
 165 170 175  
 Phe Gly Gln Ser Arg Leu Thr Val Leu Glu Ala Leu Gly Gly Ala Gly  
 180 185 190  
 Glu Arg Val Thr Thr Gln Ile Ala Ala Arg Phe Met Leu Gly Leu Val  
 195 200 205  
 His Pro Leu Asn Val Cys Ala Ile Glu Val Ala Ala Asp Glu Gly Ala  
 210 215 220  
 Arg Ile Leu Pro Leu Ala Ala Gly Arg Asp Asp Ala Leu Phe Glu His  
 225 230 235 240  
 Asp Gly Gln Ile Thr Lys Arg Glu Val Arg Ala Leu Thr Leu Ser Ala  
 245 250 255  
 Leu Ala Pro Arg Lys Gly Glu Leu Leu Trp Asp Ile Gly Gly Ser  
 260 265 270  
 Gly Ser Ile Gly Ile Glu Trp Met Leu Ala Asp Pro Thr Met Gln Ala  
 275 280 285  
 Ile Thr Ile Glu Val Glu Pro Glu Arg Ala Ala Arg Ile Gly Arg Asn  
 290 295 300  
 Ala Thr Met Phe Gly Val Pro Gly Leu Thr Val Val Glu Gly Glu Ala  
 305 310 315 320  
 Pro Ala Ala Leu Ala Gly Leu Pro Gln Pro Asp Ala Ile Phe Ile Gly  
 325 330 335  
 Gly Gly Ser Glu Asp Gly Val Met Glu Ala Ala Ile Glu Ala Leu  
 340 345 350  
 Lys Ser Gly Gly Arg Leu Val Ala Asn Ala Val Thr Thr Asp Met Glu  
 355 360 365  
 Ala Val Leu Leu Asp His His Ala Arg Leu Gly Gly Ser Leu Ile Arg  
 370 375 380  
 Ile Asp Ile Ala Arg Ala Gly Pro Ile Gly Gly Met Thr Gly Trp Lys  
 385 390 395 400  
 Pro Ala Met Pro Val Thr Gln Trp Ser Trp Thr Lys Gly  
 405 410

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 762 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: Pseudomonas denitrificans
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:

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- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobM
- (B) LOCATION: 7172-7930 bp of SEQ ID NO: 2
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATGACGGTAC	ATTTCATCGG	CGCCGGCCCG	GGAGCCGCAG	ACCTGATCAC	GGTGCCTGGT	60
CGCGACCTGA	TCGGGCGCTG	CCCGGTCTGC	CTTTACGCCG	GCTCGATCGT	CTCGCCGGAG	120
CTGCTGCGAT	ATTGGCCGCC	GGGGCCCGGC	ATTGTCGATA	CGGGCGCCGAT	GTCCCTCGAC	180
GAGATCGAGG	CGGAGATATGT	GAAGGCCGAA	GCCGAAGGGC	TCGACGTGGC	GCGGCTTCAT	240
TCGGGGACCC	TTTCGGTCTG	GAGTGCTGTG	GCCGAACAGA	TCCGCCGGCT	CGAGAACAT	300
GGCATCGCCT	ATACGATGAC	GCCGGGGCGTT	CCTTCCTTTG	CGGCGGCGGC	TTCAGCGCTC	360
GGTCGCGAAT	TGACCATTCC	GGCCGTGGCC	CAGAGCCTGG	TGCTGACCCG	CGTTTCGGGC	420
CGCGCTCGC	CGATGCCGAA	CTCAGAAACG	CTTTCGCTT	TCGGCGCTAC	GGGATCGACG	480
CTGGCAATCC	ACCTTGCAT	CCATGCGCTT	CAGCAGGTGG	TCGAGGAACT	GACGCCGCTC	540
TACGGTGCCG	ACTGCCCCGT	CGCCATCGTC	GTCAAGGCCT	CCTGGCCGGA	CGAACGCGTG	600
GTGCGCGGCA	CGCTCGGTGA	CATCGCCGCC	AAGGTGGCGG	AAGAGCCGAT	CGAGCGCACG	660
GCGCTGATCT	TCGTCGGTCC	GGGGCTCGAA	GCCTCCGATT	TCCGTGAAAG	CTCGCTCTAC	720
GATCCCGCCT	ATCAGCGGCG	CTTCAGAGGG	CGCGGCCGAAT	AG		762

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBM
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Thr Val His Phe Ile Gly Ala Gly Pro Gly Ala Ala Asp Leu Ile  
1 5 10 15

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Thr Val Arg Gly Arg Asp Leu Ile Gly Arg Cys Pro Val Cys Leu Tyr  
 20 25 30  
 Ala Gly Ser Ile Val Ser Pro Glu Leu Leu Arg Tyr Cys Pro Pro Gly  
 35 40 45  
 Ala Arg Ile Val Asp Thr Ala Pro Met Ser Leu Asp Glu Ile Glu Ala  
 50 55 60  
 Glu Tyr Val Lys Ala Glu Ala Glu Gly Leu Asp Val Ala Arg Leu His  
 65 70 75 80  
 Ser Gly Asp Leu Ser Val Trp Ser Ala Val Ala Glu Gln Ile Arg Arg  
 85 90 95  
 Leu Glu Lys His Gly Ile Ala Tyr Thr Met Thr Pro Gly Val Pro Ser  
 100 105 110  
 Phe Ala Ala Ala Ala Ser Ala Leu Gly Arg Glu Leu Thr Ile Pro Ala  
 115 120 125  
 Val Ala Gln Ser Leu Val Leu Thr Arg Val Ser Gly Arg Ala Ser Pro  
 130 135 140  
 Met Pro Asn Ser Glu Thr Leu Ser Ala Phe Gly Ala Thr Gly Ser Thr  
 145 150 155 160  
 Leu Ala Ile His Leu Ala Ile His Ala Leu Gln Gln Val Val Glu Glu  
 165 170 175  
 Leu Thr Pro Leu Tyr Gly Ala Asp Cys Pro Val Ala Ile Val Val Lys  
 180 185 190  
 Ala Ser Trp Pro Asp Glu Arg Val Val Arg Gly Thr Leu Gly Asp Ile  
 195 200 205  
 Ala Ala Lys Val Ala Glu Glu Pro Ile Glu Arg Thr Ala Leu Ile Phe  
 210 215 220  
 Val Gly Pro Gly Leu Glu Ala Ser Asp Phe Arg Glu Ser Ser Leu Tyr  
 225 230 235 240  
 Asp Pro Ala Tyr Gln Arg Arg Phe Arg Gly Arg Gly Glu  
 245 250

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4748 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: Pseudomonas denitrificans
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:Nucleotide Sequence of the 5' to 3' strand from the 4748 bp SalI-SalI-SalI-SalI-SalI-BglI fragment of Pseudomonas denitrificans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GTGCACGAGT	ATGGTCAGGT	TCAGGGTCTG	GTGACGCTGG	AGGACATTCT	GGAGGAGATC	60
GTGGCGATA	TCGCCGATGA	GCACGCCCTC	GACATTCAAG	GCGTGCGCCA	GGAAGCCGAT	120
GGCTCGATCG	TCGTCGATGG	CTCGTGCCTG	ATCCGCGATC	TCAACCGCGC	GCTCGACTGG	180
TCGCTGCCGG	ACGAGGAGGC	GACGACGGTG	GCCGGTCTGG	TCATCCACGA	GTCCAAGAGC	240
ATTCCGGAGG	AGCGCCAGGC	CTTCACCTTC	CACGGAAAC	GCTTCATCGT	GATGAAGCGG	300
GTGAAGAAC	GCATTACCAA	GCTGCCATC	CGTCCGGCGG	AAGAGGGTGC	TCCGCCGGCG	360
TGATGCCGC	GATTGCCCT	ACCAGCGGGT	CGGCTCGCCG	GGGGCTGCCG	GCTCGACGGC	420
GAGCGCATGC	AGGCCGGCGT	CGAGTTCTGG	CTTCAGGAGA	TCATTGATGG	CGCGGTGGCG	480
GGCGACACGG	CTCATGCCGG	CAAAGGCCT	AGAAACGATA	CGCACCCGCA	TGTGGACTC	540
GCCGGTACCA	TCGAAGCCCG	GCTGATGCC	GGTATGCTGA	TGGCTCTCGT	TGATGACCTC	600
GAGCGTTCA	GGGTGGAAGG	CCTCGATCAG	CTTCTTTTG	ATGGTCTCGG	TGAGCGACAT	660
TCTTCGTC	CATTTGCTG	TTTGCTTGGC	GCCCCCTCGC	AGTTAAGAAC	CCGTTAATCG	720
CTGGCACGGC	GGCGCAAAT	GCCCACAA	AGCCAGAAC	ATTCGCTTT	GTCAATTCTT	780
GTTGTGACTC	CCGCCAAACC	CCATAATGAG	CGCCATGAGA	CTCGATTCAA	AATACTTCGA	840
TCGCATTCGA	ACCCGGCGCA	AGGTGAGGCC	GCAGCAGAGC	CGGGGCTCC	CGTCTGTCAG	900
TGGGACGGCT	GCGATCAGAA	GGGTGTCAC	CGGGCGCCCG	TCGGTGCAC	CGCCGAGGGG	960
CACTACTTC	TGTTCTGCTT	CGAGCACGTG	AAGGAATACA	ACAAGGGCTA	CAACTTCTTC	1020
TCCGGCTCT	CCGACAGCGA	GGTCGCCCCG	TACCAAGAAGG	AAGCGATCAC	CGGTATCGG	1080
CCCACCTGGA	CCGTCCGGCT	CAACAAAGAC	GCCAAGAACG	GCCCCACCCA	GTGGCAGACG	1140
CGGTCTGGCT	CTGCCGGCGC	CCAGGCCCGC	ATGCGCGATC	CCTTGGCTT	TGTCAGCGAG	1200
GCGCGGGCGC	GATCCGGTCG	TCCCAGGCCA	CGCCAGCGCA	AGCTGAAGAC	GCTCGAGGCG	1260
AAGGCCTTCG	AAACGCTTGG	TCTCGAGCC	TCGGCGACCA	CTGGCGACAT	CAAGGGGCC	1320
TACAAGGACC	TCGTCAGAA	GCATCACCCC	GATGCCAATG	GCGGAGATAG	AGGATCGGAA	1380
GAGCGTTTC	GGCGGGTTAT	TCAGGCCTAC	CAATTGTTAA	AACAGGCTGG	TTTCTGCTAA	1440
CAACCCGGAT	TAATACAGAA	GCACCTTTCG	AGGCGAATGC	GCGGGTGC	TCCGGTGGCC	1500
GCTCTGGAGA	CATGATGAGC	AAGATTGACC	TCGACATTT	CAACCTCCCC	GACACCACGA	1560
TTTCCGTCG	GGAGGTTTT	GGTATTGATA	CGGATTGCG	CGTTCTGCC	TATTGAAAGG	1620
GCGACGCC	TGTCCGGAT	CTGGATCCGG	ACTACCTTT	CGACCGCGAA	ACGACGCTCG	1680
CCATTCTCGC	AGGCTTCGCC	CACAACCGAC	CGGTGATGGT	GTCGGGCTAT	CACGGCACCG	1740
GCAAGTCCAC	CCATATCGAG	CAGGTGCGCG	CGCGCTCAA	CTGGCGTGC	GTGCGCGTCA	1800
ACCTCGATAG	CCATGTCAGC	CGTATCGACC	TCGTCGGAA	GGACGCGATC	GTCGTCAAGG	1860
ACGGCCTGCA	GGTCACCGAA	TTCAAGGACG	GCATCTGCC	CTGGGCTAC	CAGCACAATG	1920
TCGCCTCGT	CTTCGACGAA	TACGATGCCG	GCCGCCCGGA	CGTCATGTT	GTCATCCAGC	1980
GCGTGTGGA	ATCCTCCGGC	CGCCTGACGC	TGCTCGACCA	GAGCGTGTG	ATCCGTCGCC	2040
ACCCGGCTT	CCGCCTGTTT	GCACCGCCA	ACACCGTGG	CCTCGGCAC	ACGACCGGCC	2100
TCTATCACGG	CACCGAGCAG	ATCAACCGG	CGCAGATGGA	CGCGATGGT	ATCGTCACCA	2160
CGCTGAACTA	CCTGCCGAC	GACAAGGAAG	TCGACATCGT	CGCCGCCAAG	GTCAAGGGCT	2220
TCACCGCCGA	CAAGGGCCG	GAGACCGTCT	CCAAGATGGT	ACGTGTCGCC	GACCTCACGC	2280
GCGCAGCCTT	CATCAATGGC	GATCTCGA	CTGTATGAG	CCCGCGTACG	GTCATCACCT	2340
GGGCCGAGAA	CGCCCCACATC	TTCGCGACA	TCGCTTTCG	CTTCCGCGTG	ACCTTCCTCA	2400
ACAAGTGC	CGAGCTGGAG	CGGGCGCTGG	TCGCCAGCA	CTACCAAGCGC	GCCTTCGGCA	2460
TCGAGCTGAA	GGAATGCGCT	GCCAAACATCG	TGCTCGAAGC	CACCGCCTGA	TCCCACGGCC	2520
TGCCGTCCCC	TTTGGGAGGG	CGGGTCATGA	CGCTGTGGCA	AACCGGATGA	CGCCCCACTG	2580
GGGCGCCGTC	GCCTCTGGCT	GAAGAAGGA	CTGCTGTGAG	CTCGAATTG	AAGGCAAAGC	2640
CAACCAACGCG	CGAGAAATGCT	GCAGGAACCGT	TCAAGCGGCC	GCTTCCGGC	TGCATCCGAT	2700
CGATCGCGGG	CGATGCCGAG	GTGGAAGTCG	CCTTCGCAA	CGAGCGGCCG	GGCATGACCG	2760
GCGAACGCA	CCGTCTGCCG	GAACCTTCCA	AGCGCCCGAC	CCTGCAGGAA	CTTGCCTGTA	2820
CCCGCGGGCT	CGGTGACAGC	ATGGCGCTGC	GCAAGGCTG	TACGCATGCC	CGGATCCAGC	2880
GCACCATGTC	GGCGCAAGGG	GGGGACGCC	CGCGATCTT	CGATGCGGTG	GAGCAGGCTC	2940
GTGTCGAGGC	GATCGGTGCG	TTGCGCATGG	CGGGTGTGCG	CAAGAACCTC	AACGTATGC	3000
TCGAAGAGAA	ATACGCCAAG	GCGAATTTCG	CAACGATCGA	CGCCAGGCCG	GACGCGCCGC	3060
TCGGCGAGGC	CGTAGCGCTG	CTGGTGCCTG	AGAAGCTGAC	GGGGCAGAAG	CCGCGCGCGT	3120
CTGCCGGCAA	GGTGTCTGAC	CTCTGGCG	AGTTCATCGA	GGGCAAGGCT	GCCGGCGACA	3180
TTGAGCACCT	GTCGTCGACG	ATCAACAAACC	AGCAGGCC	TGCCCCGGTC	GTTCGCGACA	3240
TGCTGACCTC	GATGGAAGTC	GCCGAGAAAT	ACGGTGACGA	CGACAACGAG	CCGGACGAGC	3300
AGGAAAGCGA	GACCGACGAA	GACCGCCG	CGAGCCAGGA	GCAGGACGAG	AACGCCAGCG	3360
ACGAGGAAGC	CGGCGACGAT	GCCGCACCCG	CCGACGAGAA	CCAGGCTGCC	GAAGAGCAGA	3420
TGGAAGAAGG	CGAGATGGAC	GGCGCGGAGA	TCTCCGACGA	CGATCTCCAG	GACGAAGGCG	3480
ACGAGGACAG	CGAAACGCCC	GGCGAGGTCA	AGCGTCCGAA	CCAGCCCTTC	GCGACTTCA	3540
ACGAGAAGGT	CGACTACGCC	GTCTCACCC	GCGAGTTCGA	CGAGACGATT	GCCTCGGAAG	3600

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AGCTTTCGCA	CGAGGCCGAG	CTCGACCGGC	TGCGCGCCTT	CCTCGACAAG	CAGCTTGCCTC 3660
ATCTTCAGG	CGCGGTCGGC	CGCCTTGCCA	ACCGGCTGCA	GCGCCGCCTG	ATGGCGCAGC 3720
AGAACCGCTC	CTGGGAGTTTC	GATCTCGAAG	AGGGGTATCT	CGATTGCGCG	CGGCTTCAGC 3780
GCATCATCAT	CGATCCGATG	CAGCCGCTTT	CCTTCAAGCG	CGAAAAGGAC	ACCAACTTCC 3840
GCGATACCGT	CGTGACGCTG	CTGATCGACA	ATTCCGGCTC	GATGCGCGGC	CGTCCGATCA 3900
CGGTTGCCGC	CACCTGCGCC	GATATCCTGG	CGCGCACGCT	CGAGCGCTGC	GGCGTCAAGG 3960
TCGAGATCCT	CGGTTTTACC	ACCAAGGCGT	GGAAAGGGTGG	GCAGTCACGC	GAGAAGTGGC 4020
TGGCCGGCGG	CAAGGCCACAG	GCCCCGGGTC	GCCTCAACGA	CCTGCGACAC	ATCGTCTACA 4080
AGTCTGCCA	CGCTCCGTGG	CGCCGGGCAC	GACGCAATCT	CGGCGTGTATG	ATGCGGGAAAG 4140
GCCTGCTCAA	GGAAAACATC	GACGGCGAGG	CGTTGATTG	GGCGCATGAG	CGGCTGATGG 4200
CGCGGGCGA	ACAGCGGCGC	ATCCTGATGA	TGATTTCGGA	CGGCGCGCCG	GTCGACGACT 4260
CGACGCTGTC	GGTCAATCCA	GGAAACTATC	TGGAGCGTCA	CCTGCGCGCG	GTCATCGAGC 4320
AGATGAAAC	GCGCTCGCCG	GTGGAACACTG	TGGCGATCGG	TATCGGCCAC	GACGTGACGC 4380
GCTACTATCG	CCGTGCCGTC	ACCATCGTCG	ATGCCGATGA	GCTTGCCTGGC	GCGATGACCG 4440
AACAGCTGGC	CGCACTCTTC	GAGGACGAAA	GCCAGCGCCG	CGGTTCTTCG	CGTCTTCGCC 4500
GCGCCGGGTG	ATGCTTCCCC	CTTGGGGGCG	GTGGAACATC	GCCTCCGAGC	TGCCAATCGG 4560
CACCTGCACG	CATCGCTGGC	GGCCGAAGTC	AATTTACGGA	CATAGTTTA	CAGTCTACCA 4620
AGTACCATG	CGTGGCGGGC	TCACTTTGAG	CGCACGCCGC	GTCATTCCCG	ATGCCCCCTG 4680
AAGGTACTTC	TCTTGATGCT	TGGCCGCGGT	CTCCTAGCCC	TTTCCCTCCT	GGCTTCGGCC 4740
TGCCCGGC					4748

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3855 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: Pseudomonas denitrificans
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Nucleotide Sequence of the 5' to 3' strand from the 3855 bp SstI-SstI-BamHI fragment of Pseudomonas denitrificans
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

GAGCTCATAG	AGCAGTTCT	CGATCGACTT	CAGCAGTCGC	ATGAAATCCA	TGCCGTGCTC 60
CCCTTGCTTC	TATGCGTGGC	ACGACCGCGC	GCCGGGGCCG	ATGCCGGTCA	GTCGCGCAGA 120
CGCAGCTCGT	CGGTACGCAT	CTGCAGCATC	TCCAGCGTCG	ACAGGAAGCT	CATGCCGAGC 180
AGGCTCTGAT	CGAGCTTGCC	CTTGGCTGCG	ACCGTTGCGC	CGATGTTGCG	GCGGGTGATC 240
GGGCCGATCG	AGATCTCTG	AAGCATCACG	GGGGCTGCC	GGGCCCGGCC	ATTGGCTGTC 300
ATGACCGTGA	CGATAAAAGTT	GAGGTTGGCC	GGGTGAGGGC	CGATCTTTC	CGCATCTTCA 360
TAGGTGAGCG	CGATGTTGCT	GGGCCGGTA	TCGACCAGCA	TGCTGATGTC	CTTGCCGTG 420
ACCGTCGCA	TGGTCTCGAA	ATGACCGTTC	AGCATCTTCT	GCAGCACCAC	TTCCCTGCTGT 480

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CCCTCGCTGT	CAGTGATGAT	GGTGGCGCGG	CCGGGGATGA	GGCCGGCGAG	CAGGCAGGTTA	540		
CCGAAGCCCT	CCAACTCGAA	GCGGTAGACA	TAGGCCGAGA	CCAGCGCCAG	AACGACGAAG	600		
AGCCAGATGG	CGATCTGACG	CAGGCCCTCG	CCGAAGCGGT	GGCGGCTCTG	CAGGATGCCG	660		
GCGCCGATCA	GCGTGGCGAT	GGCGCCGAGC	GAGACCAAGT	GCCCCGACTG	GTCATTGGCA	720		
AGCCCCATGG	TGCGGCCGGT	GTCGTGGTTG	ATGATCAGCA	GGATGAGGCC	GATGGCCAGG	780		
ATCGAGAGCA	GGATGGCAAG	ACGGGTATG	CTTCGCCGCG	TTCCCTCGCC	ATGCGCGTGC	840		
GTCGGGTTTC	GCGCCGCGGC	TTGCGTTCGA	CGGTCTCAAG	CCGTGCAGGC	AACGCGCTCA	900		
TGATCGCGCG	GCGTTCGGCA	TCGGTATAGA	GCGTCCAGCG	TCCGACTTCG	TCGCGGGTAC	960		
GGCCGCCAGCC	GAAACAGTAG	CCGGTCTTGT	CATCGATCGA	ACAGACGAGA	ATGCAGGGAG	1020		
ATTCCATGGG	CGTGTCAAGT	TTTCCCTTGA	TATATCGATG	TTTCAAACCG	TCAGCGCAAG	1080		
GGCACCGAGC	ACGGCGATT	CGGTCAAGTTG	CTGCGTCGCC	CCGATCGTGT	CGCCCCGTTG	1140		
TCCGCCGATC	TTGCGCATCG	CCAGGCCGAGC	GAAGCCCTTG	ACCGTGGCAA	GAATGCGAC	1200		
GAGGCCCGCG	ATGACGCCGA	GCGCCGGGAC	CTGCGCGAGA	TAGAAGAGCA	GCATTGCGAC	1260		
AAGAAAGTCCG	AAGGCAAGCG	CGAACGCGT	GGCCGCCGGT	TCCGGCTCGC	CAGCCGAGGC	1320		
CGCGACGCCG	CTGCTGCGC	CCGGCGGAAG	CGACGACCAAG	TGGCAGACCA	TGGCGGCCGCG	1380		
GCTGAGGCAC	GCTGCGCCAA	GGATCGCCAT	GGCGGCCGCC	AGCGGCAGAA	AGAGCGGCAG	1440		
GATCGAGGCG	AACGCCGAGA	CGCCGAGGCC	GAAGGAGAGG	ATGAGGGCGA	CGGCCGCATA	1500		
GGTCCCGATG	GGGCTCTC	TCATGATCGC	AAGGCCGCGT	TCGGGTCGCC	GACGCCGCC	1560		
AAAGCCATCG	GCCGTGTTCG	CAAGGCCGTC	TTCTGTCACT	GCGCCGGTGA	CAAGCGCTG	1620		
GATGGCGACG	ACGACAAAGG	CGGCAAAGAG	CGAGCTCACC	TGCAAGCGCA	TGAGGGCAT	1680		
GGCGACGGCC	GCGATGGCA	GTGCGATCGC	CAGGCCGGCG	AAACGGGAAGG	CGCGCACGGC	1740		
ACGGCTCAAG	CGCCCCGTCA	AACCTTCGAA	ATGACCGCA	GGCATCGGGA	TGCGGCTGAG	1800		
AAAGCCGATC	GAACCGCGCA	CATCGTCACA	GAATCGCCA	ACGAAGCCCA	TGGCTCCTCC	1860		
AAGGTTGCGG	CAATTGACCC	GGCCGCTGCC	AAACTCGCCG	ACTGCGGCGA	GTCTCGCAAG	1920		
CCGGGCGGGC	GCACCCCGCA	GGGCCGCGCA	CACTTTTCCC	AGACCTTTCA	TAGGCCGTCT	1980		
GCGACCGCTC	GGGGATCGAG	ACGGGACGCG	CGATTGGCGC	AAATGTCGTT	GCCCGAATT	2040		
TCGGGCCCT	CTATGAGGGG	CGTAGATAGA	GCTTCACGAT	GATGCAAGGA	TTCTCCCAT	2100		
GAGTGCCAGC	GGCCTGCCGT	TTGATGATTT	TCGCGAATTG	TTGCGCAACC	TGCCGGGCC	2160		
GGATGCGGCA	GCCCTCGTTG	CCGCGCGGGG	CGGGGACGCC	CAGCTGACGA	AGCCGCCGGG	2220		
CGCGCTCGGC	CGCCTCGAGG	AAATCGCCTT	CTGGCTCGCC	GCCTGGACGG	GCAAGGCGCC	2280		
GGTGTCAAC	CGGCCGCTGG	TGGCGATCTT	TGCCGGCAAC	CACGGCGTCA	CCGCCAGGG	2340		
GGTGACCCCG	TTCCCCTCAT	CCGTCACCGC	ACAGATGGTC	GAGAATTGTTG	CCGCCGGTGG	2400		
CGCTGCGATC	AACCAGATCT	CGCTCAGCCA	CGACCTCGGG	CTGAAGGTCT	TCGACCTCGC	2460		
ACTCGAATAC	CGGACCGGTG	ATATCACCAG	GGAAAGCCGCG	CTGTCGAGC	GCGATTGCGC	2520		
CGCGACCATG	GCCTTTGGCA	TGGAGGCAGT	TGCCGGCGC	ACGGATCTTC	TGTGATCGG	2580		
CGAAATGGGC	ATCGGCAACA	CCACGATCGC	GGCCGCGATC	AATCTGGCC	TTTATGGTGG	2640		
CACGGCCGAA	GAATGGGTG	GTCCGGGTAC	CGGCTCCGAG	GGCGAGGTGC	TGAAGCGCAA	2700		
GATCGCCGCG	GTCGAAAAGG	CCGTTGGCGCT	GCATCGCGAT	CACCTGTCCG	ATCCGCTCGA	2760		
ACTGATGCGT	CGCCTCGGGC	GTCGTAGAGT	CGCGGCCATG	GCTGGCGCCA	TCCTGGCCG	2820		
CCGCGTCCAG	AAGGTACCTG	TCATCATCGA	CGGCTACGTG	CGCACCGCTG	CGGCTTCGAT	2880		
CCTGAAGGCG	GCCAACCCGT	CGGCCCTCGA	CCATTGCGCTG	ATCGGCCATG	TTTCGGCGA	2940		
ACCGGGGCAT	CTGCGCGCA	TCGAGAAGCT	CGGCAAGACG	CCGCTGCTGG	CACTCGGCAT	3000		
GGGGCTTGGC	GAAGGCACGG	GCGCGGCCCT	TGCGCCGGGT	ATCGTCAAGG	CGGCGGCCGC	3060		
TTGCCACAGC	GGCATGGCGA	CCTTTGCCA	GGCCGGCGTC	AGCAACAAGG	AATAGTGAAG	3120		
TTCCGGCCGG	GCTTTCGAGG	AAGGCCGGCC	GGTTTCTGTC	CAAGGCCCTG	CACGGCGCG	3180		
AAGCTGTCG	GTGCCGGGCC	TTGATGGATG	CGTCCTTCTC	GCCTATCCAA	AGCGAAATG	3240		
CGCGCCCTAG	CTATAGTCTT	GGGTGCCCTG	AACCGAGACC	GCCTTGATT	CGCCTCAATC	3300		
ACGATGTCGA	AGCAAGCACA	GTTCGAAGCC	CTGTCGAGAC	GAAATGGACG	CCAAGAACAC	3360		
CACGCACCGC	ATTGGACAGA	CGGGTCCCTG	CGAGAACGAG	ACCGGCATT	GGCATCTCTT	3420		
TGCCGCTCG	AGCTATTGCG	TCGGCGCGC	CAAGCGGCTG	ATCGCGAGG	CTGCCCTTCG	3480		
CCACGAGCTG	ATCGCCTTTC	CCGCCCGCGAT	GATCGTTTC	ATCATCGTCG	GCGAACCTT	3540		
CTTCCAAAT	GTGGCGATGG	CGATCCTGTT	CCTGCTGATG	ATGGCCTCG	AGGCGATCAA	3600		
CACGGCAATC	GAGGAAATTG	TCGATCGCGT	TTCTCCCGAA	ATCTCGGAAA	TGGGTAAGAA	3660		
CGCCAAGGAT	CTCGGCTCT	TCGCTGCCCT	CTGCGCTGATT	GTGCGCAACG	GTGTCTATGC	3720		
CGCCCTATGTC	GTGATCTTCG	ACGGCTTCAT	GAACGTGACCG	GCTAGCGGGC	CGGCGCTTC	3780		
ACCCGATAAA	GCACATGCGG	ACGCAGCGGG	TTGCCCCCGG	GTACCGTGAC	GTCGTCGAAA	3840		
TCATCAGCCG	GATCC					3855		

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 999 base pairs  
 (B) TYPE: Nucleic Acid

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(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas denitrificans*

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

(F) TISSUE TYPE:

(G) CELL TYPE:

(H) CELL LINE:

(I) ORGANELLE:

(ix) FEATURE:

(A) NAME/KEY: cobs

(B) LOCATION: 1512-2510 bp of SEQ ID NO: 29

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGATGAGCA	AGATTGACCT	CGACATTCC	AACCTCCCCG	ACACCACGAT	TTCCGTCCGG	60
GAGGTTTTCG	GTATTGATAC	GGATTGCGC	GTTCTGCCT	ATTGAAAGGG	CGACGCCAT	120
GTCCCGGATC	TGGATCCGGA	CTACCTCTTC	GACCGCGAAA	CGACGCTCGC	CATTCTCGCA	180
GGCTTCGCC	ACAACCGACG	CGTGATGGTG	TGGGGCTATC	ACGGCACCGG	CAAGTCCACC	240
CATATCGAGC	AGGTGCGCCG	GCGCCTCAAC	TGGCCGTGCG	TGCGCGTCAA	CCTCGATAGC	300
CATGTGAGCC	GTATGACCT	CGTCGGCAAG	GACGCGATCG	TCGTCAGGA	CGGCCTGCAG	360
GTCACCGAAT	TCAAGGACGG	CATCCTGCC	TGGGCCTACC	AGCACAAATGT	CGCGCTCGTC	420
TTCGACGAAT	ACGATGCCGG	CCGCCCGGAC	GTCATGTTCG	TCATCCAGCG	CGTGCTGGAA	480
TCCTCCGGCC	GCCTGACGCT	GCTGACCGAG	AGCCGTGTC	TCCGTCGGCA	CCCGGCCCTTC	540
CGCCTGTTG	CGACCGCCAA	CACCGTCGGC	CTCGCGACA	CGACCGGGCT	CTATCACGGC	600
ACGCAAGAGA	TCAACCGAGG	GCAGATGGAC	CGCTGGTCGA	TCGTCACCAAC	GCTGAACATAC	660
CTGCCGACG	ACAAGGAAGT	CGACATCGTC	GCCGCCAAGG	TCAAGGGCTT	CACCGCCGAC	720
AAGGGCCGCG	AGACCGTCTC	CAAGATGGTA	CGTGTGCGCG	ACCTCACGCG	CGCAGCCCTTC	780
ATCAATGGCG	ATCTCTCGAC	TGTGATGAGC	CCGCGTACGG	TCATCACCTG	GGCCGAGAAC	840
GCCCCACATCT	TGGCGACAT	CGCTTCGCG	TTCCGCGTGA	CCTTCCTCAA	CAAGTGCAG	900
GAGCTGGAGC	GGGCGCTGGT	CGCCGAGCAC	TACCAAGCGCG	CCTTCGGCAT	CGAGCTGAAG	960
GAATGCGCTG	CCAACATCGT	GCTCGAAGGCC	ACCGCCTGA			999

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: Amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas denitrificans*

(B) STRAIN:

(C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:

(E) HAPLOTYPE:

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- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBS
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:31

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Met Ser Lys Ile Asp Leu Asp Ile Ser Asn Leu Pro Asp Thr Thr  
1 5 10 15  
Ile Ser Val Arg Glu Val Phe Gly Ile Asp Thr Asp Leu Arg Val Pro  
20 25 30  
Ala Tyr Ser Lys Gly Asp Ala Tyr Val Pro Asp Leu Asp Pro Asp Tyr  
35 40 45  
Leu Phe Asp Arg Glu Thr Thr Leu Ala Ile Leu Ala Gly Phe Ala His  
50 55 60  
Asn Arg Arg Val Met Val Ser Gly Tyr His Gly Thr Gly Lys Ser Thr  
65 70 75 80  
His Ile Glu Gln Val Ala Ala Arg Leu Asn Trp Pro Cys Val Arg Val  
85 90 95  
Asn Leu Asp Ser His Val Ser Arg Ile Asp Leu Val Gly Lys Asp Ala  
100 105 110  
Ile Val Val Lys Asp Gly Leu Gln Val Thr Glu Phe Lys Asp Gly Ile  
115 120 125  
Leu Pro Trp Ala Tyr Gln His Asn Val Ala Leu Val Phe Asp Glu Tyr  
130 135 140  
Asp Ala Gly Arg Pro Asp Val Met Phe Val Ile Gln Arg Val Leu Glu  
145 150 155 160  
Ser Ser Gly Arg Leu Thr Leu Leu Asp Gln Ser Arg Val Ile Arg Pro  
165 170 175  
His Pro Ala Phe Arg Leu Phe Ala Thr Ala Asn Thr Val Gly Leu Gly  
180 185 190  
Asp Thr Thr Gly Leu Tyr His Gly Thr Gln Gln Ile Asn Gln Ala Gln  
195 200 205  
Met Asp Arg Trp Ser Ile Val Thr Thr Leu Asn Tyr Leu Pro His Asp  
210 215 220  
Lys Glu Val Asp Ile Val Ala Ala Lys Val Lys Gly Phe Thr Ala Asp  
225 230 235 240  
Lys Gly Arg Glu Thr Val Ser Lys Met Val Arg Val Ala Asp Leu Thr  
245 250 255  
Arg Ala Ala Phe Ile Asn Gly Asp Leu Ser Thr Val Met Ser Pro Arg  
260 265 270  
Thr Val Ile Thr Trp Ala Glu Asn Ala His Ile Phe Gly Asp Ile Ala  
275 280 285  
Phe Ala Phe Arg Val Thr Phe Leu Asn Lys Cys Asp Glu Leu Glu Arg  
290 295 300  
Ala Leu Val Ala Glu His Tyr Gln Arg Ala Phe Gly Ile Glu Leu Lys  
305 310 315 320  
Glu Cys Ala Ala Asn Ile Val Leu Glu Ala Thr Ala  
325 330

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1896 base pairs
- (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas denitrificans*  
(B) STRAIN:  
(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:

(A) NAME/KEY: cobT  
(B) LOCATION: 2616-4511 bp of SEQ ID NO: 29  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GTCGAGCTCGA	ATTCGAAGGC	AAAGCCAACC	ACGCGCGAGA	ATGCTGCGGA	ACCGTTCAAG	60
CGGGCGCTTT	CCGGCTGCAT	CCGATCGATC	CGGGGCGATG	CCGAGGTGGA	AGTCGCCTTC	120
GCCAACGAGC	GGCCGGGCAT	GACCGGCGAA	CGCATCCGTC	TGCCGGAACT	TTCCAAGCGC	180
CCGACCCCTGC	AGGAACCTTG	CGTGACCCGC	GGGCTCGTG	ACAGCATGGC	GCTGCGAAG	240
GCCTGTACGC	ATGCGCGGAT	CCAGCGCACC	ATGTCGCCGC	AAGGGGCGGA	CGCCCGCGCG	300
ATCTTCGATG	CGGTGGAGCA	GGCTCGTGT	GAGGCGATCG	GGTCGTTGCG	CATGGCGGGT	360
GTCGCCAAGA	ACCTCAACGT	CATGCTCGAA	GAGAAATACG	CCAAGGCGAA	TTTCGCAACG	420
ATCGAGCGCC	AGGCGGACGC	GCCGCTCGGC	GAGGCCGTAG	CGCTGCTGGT	GCGCGAGAAG	480
CTGACGGGCC	AGAACCGGCC	GGCGCTCTGC	GGCAAGGTGC	TCGACCTCTG	GCGCGAGTT	540
ATCGAGGGCA	AGGCTGCCGC	CGACATTGAG	CACCTGTCGT	CGACGATCAA	CAACAGCAG	600
GCCTTTCGCCC	GGGTCGTTCG	CGACATGCTG	ACCTCGATGG	AAGTCGCCGA	GAAATACGGT	660
GACGACGACA	ACGAGCCGGA	CGAGCAGGAA	AGCGAGACCG	ACGAAGACCA	GCGCGCAGC	720
CAGGAGCAGG	ACGAGAACGC	CAGCGACGAG	GAAGCCGGCG	ACGATGCCGC	ACCCGCCGAC	780
GAGAACCAAGG	CTGCCGAAGA	GCAGATGGAA	GAAGGCAGAGA	TGGACGGCGC	GGAGATCTCC	840
GACGACGATC	TCCAGGACGA	AGGGCAGCAG	GACAGCGAAA	CGCCCGGCGA	GGTCAAGCGT	900
CCGAACCAGC	CCTTCGCGGA	CTTCAACGAG	AAGGTCGACT	ACGCCGTCTT	CACCCGGAG	960
TTCGACGAGA	CGATTGCCTC	GGAAGAGCTT	TGCGACGAGG	CCGAGCTCGA	CCGGCTGCGC	1020
GCCTTCTCTG	ACAAGCAGCT	TGCCCATCTT	CAAGGCGCGG	TCGGCCGCGCT	TGCCAACCAG	1080
CTGCAGCGCC	GCCTGATGGC	GCAGCAGAAC	CGCTCTGGG	AGTTGATCT	CGAAGAGGGG	1140
TATCTCGATT	CGGCGCGGCT	TCAGCGCATC	ATCATCGATC	CGATGCAGCC	GCTTTCCTTC	1200
AAGCGCGAAA	AGGACACCAA	CTTCCGCGAT	ACCGTCGTGA	CGCTGCTGAT	CGACAATTCC	1260
GGCTCGATGC	GGGGCGCTCC	GATCACGGTT	GCCGCCACCT	GCGCCGATAT	CCTGGCGCGC	1320
ACGCTCGAGC	GCTGCGGCGT	CAAGGTCGAG	ATCCTCGTT	TTACCACCAA	GGCGTGGAAG	1380
GGTGGGCAGT	CACGCGAGAA	GTGGCTGGCC	GGCGGCAAGC	CACAGGCC	GGGTCGCCCTC	1440
AACGACCTGC	GACACATCGT	CTACAAAGTCT	GCCGACGCTC	CGTGGCGCCG	GGCACGACGC	1500
AATCTCGGCC	TGATGATGCG	GGAAAGGCTG	CTCAAGGAAA	ACATCGACGG	CGAGGCGTTG	1560
ATTGGGGCGC	ATGAGCGGCT	GATGGCGCGG	CGCGAACAGC	GGCGCATCCT	GATGATGATT	1620
TCGGACGGCG	CGCCGGTCGA	CGACTCGACG	CTGTCGGTCA	ATCCAGGAAA	CTATCTGGAG	1680
CGTCACCTGC	GGCGGGTCAT	CGAGCAGATC	GAAACGCGCT	CGCCGGTGA	ACTGCTGGCG	1740
ATCGGTATCG	GCCACGACGT	GACCGCGCTAC	TATCGCGT	CCGTCACCAT	CGTCGATGCC	1800
GATGAGCTTG	CCGGCGCGAT	GACCGAACAG	CTGGCCGAC	TCTTCGAGGA	CGAAAGCCAG	1860
CGCCGCGGTT	CTTCGCGTCT	TCGCGCGGCC	GGGTGA			1896

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 631 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBT
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Val Ser Ser Asn Ser Lys Ala Lys Pro Thr Thr Arg Glu Asn Ala Ala  
1 5 10 15  
Glu Pro Phe Lys Arg Ala Leu Ser Gly Cys Ile Arg Ser Ile Ala Gly  
20 25 30  
Asp Ala Glu Val Glu Val Ala Phe Ala Asn Glu Arg Pro Gly Met Thr  
35 40 45  
Gly Glu Arg Ile Arg Leu Pro Glu Leu Ser Lys Arg Pro Thr Leu Gln  
50 55 60  
Glu Leu Ala Val Thr Arg Gly Leu Gly Asp Ser Met Ala Leu Arg Lys  
65 70 75 80  
Ala Cys Thr His Ala Arg Ile Gln Arg Thr Met Ser Pro Gln Gly Ala  
85 90 95  
Asp Ala Arg Ala Ile Phe Asp Ala Val Glu Gln Ala Arg Val Glu Ala  
100 105 110  
Ile Gly Ser Leu Arg Met Ala Gly Val Ala Lys Asn Leu Asn Val Met  
115 120 125  
Leu Glu Glu Lys Tyr Ala Lys Ala Asn Phe Ala Thr Ile Glu Arg Gln  
130 135 140  
Ala Asp Ala Pro Leu Gly Glu Ala Val Ala Leu Leu Val Arg Glu Lys  
145 150 155 160  
Leu Thr Gly Gln Lys Pro Pro Ala Ser Ala Gly Lys Val Leu Asp Leu  
165 170 175  
Trp Arg Glu Phe Ile Glu Gly Lys Ala Ala Gly Asp Ile Glu His Leu  
180 185 190  
Ser Ser Thr Ile Asn Asn Gln Gln Ala Phe Ala Arg Val Val Arg Asp  
195 200 205  
Met Leu Thr Ser Met Glu Val Ala Glu Lys Tyr Gly Asp Asp Asp Asn  
210 215 220  
Glu Pro Asp Glu Gln Glu Ser Glu Thr Asp Glu Asp Gln Pro Arg Ser  
225 230 235 240  
Gln Glu Gln Asp Glu Asn Ala Ser Asp Glu Glu Ala Gly Asp Asp Ala  
245 250 255  
Ala Pro Ala Asp Glu Asn Gln Ala Ala Glu Glu Gln Met Glu Glu Gly

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260	265	270													
Glu	Met	Asp	Gly	Ala	Glu	Ile	Ser	Asp	Asp	Asp	Leu	Gln	Asp	Glu	Gly
275			280			285									
Asp	Glu	Asp	Ser	Glu	Thr	Pro	Gly	Glu	Val	Lys	Arg	Pro	Asn	Gln	Pro
290			295			300									
Phe	Ala	Asp	Phe	Asn	Glu	Lys	Val	Asp	Tyr	Ala	Val	Phe	Thr	Arg	Glu
305			310			315			320						
Phe	Asp	Glu	Thr	Ile	Ala	Ser	Glu	Glu	Leu	Cys	Asp	Glu	Ala	Glu	Leu
				325			330			335					
Asp	Arg	Leu	Arg	Ala	Phe	Leu	Asp	Lys	Gln	Leu	Ala	His	Leu	Gln	Gly
				340			345			350					
Ala	Val	Gly	Arg	Leu	Ala	Asn	Arg	Leu	Gln	Arg	Arg	Leu	Met	Ala	Gln
				355			360			365					
Gln	Asn	Arg	Ser	Trp	Glu	Phe	Asp	Leu	Glu	Glu	Gly	Tyr	Leu	Asp	Ser
				370			375			380					
Ala	Arg	Leu	Gln	Arg	Ile	Ile	Ile	Asp	Pro	Met	Gln	Pro	Leu	Ser	Phe
				385			390			395					400
Lys	Arg	Glu	Lys	Asp	Thr	Asn	Phe	Arg	Asp	Thr	Val	Val	Thr	Leu	Leu
				405			410			415					
Ile	Asp	Asn	Ser	Gly	Ser	Met	Arg	Gly	Arg	Pro	Ile	Thr	Val	Ala	Ala
				420			425			430					
Thr	Cys	Ala	Asp	Ile	Leu	Ala	Arg	Thr	Leu	Glu	Arg	Cys	Gly	Val	Lys
				435			440			445					
Val	Glu	Ile	Leu	Gly	Phe	Thr	Thr	Lys	Ala	Trp	Lys	Gly	Gly	Gln	Ser
				450			455			460					
Arg	Glu	Lys	Trp	Leu	Ala	Gly	Gly	Lys	Pro	Gln	Ala	Pro	Gly	Arg	Leu
				465			470			475					480
Asn	Asp	Leu	Arg	His	Ile	Val	Tyr	Lys	Ser	Ala	Asp	Ala	Pro	Trp	Arg
				485			490			495					
Arg	Ala	Arg	Arg	Asn	Leu	Gly	Leu	Met	Met	Arg	Glu	Gly	Leu	Leu	Lys
				500			505			510					
Glu	Asn	Ile	Asp	Gly	Glu	Ala	Leu	Ile	Trp	Ala	His	Glu	Arg	Leu	Met
				515			520			525					
Ala	Arg	Arg	Glu	Gln	Arg	Arg	Ile	Leu	Met	Met	Ile	Ser	Asp	Gly	Ala
				530			535			540					
Pro	Val	Asp	Asp	Ser	Thr	Leu	Ser	Val	Asn	Pro	Gly	Asn	Tyr	Leu	Glu
				545			550			555					560
Arg	His	Leu	Arg	Ala	Val	Ile	Glu	Gln	Ile	Glu	Thr	Arg	Ser	Pro	Val
				565			570			575					
Glu	Leu	Leu	Ala	Ile	Gly	Ile	Gly	His	Asp	Val	Thr	Arg	Tyr	Tyr	Arg
				580			585			590					
Arg	Ala	Val	Thr	Ile	Val	Asp	Ala	Asp	Glu	Leu	Ala	Gly	Ala	Met	Thr
				595			600			605					
Glu	Gln	Leu	Ala	Ala	Leu	Phe	Glu	Asp	Glu	Ser	Gln	Arg	Arg	Gly	Ser
				610			615			620					
Ser	Arg	Leu	Arg	Arg	Ala	Gly									
				625			630								

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*

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- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobx
- (B) LOCATION: 4089-4370 bp of SEQ ID NO:29
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGTCGCTCA	CCGAGACCAT	CGAAAAGAAG	CTGATCGAGG	CCTTCCACCC	TGAACGGCTC	60
GAGGTCTATCA	ACGAGAGCCA	TCAGCATACC	GGCCATCAGC	CGGGCTTCGA	TGGTACCGGC	120
GAGTCCCACA	TGCGGGTGCG	TATCGTTCT	AGCGCCTTG	CCGGCATGAG	CCGTGTCGCC	180
CGCCACCGCG	CCATCAATGA	TCTCCTGAAG	CCAGAACTCG	ACGCCGGCCT	GCATCGCTC	240
GCCGTCGAGC	CGGCAGCCCC	CGGGAGCCG	ACCCGCTGGT	AG		282

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBX
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met	Ser	Leu	Thr	Glu	Thr	Ile	Glu	Lys	Lys	Leu	Ile	Glu	Ala	Phe	His
1				5				10						15	
Pro	Glu	Arg	Leu	Glu	Val	Ile	Asn	Glu	Ser	His	Gln	His	Thr	Gly	His
	20				25								30		
Gln	Pro	Gly	Phe	Asp	Gly	Thr	Gly	Glu	Ser	His	Met	Arg	Val	Arg	Ile
	35				40								45		
Val	Ser	Ser	Ala	Phe	Ala	Gly	Met	Ser	Arg	Val	Ala	Arg	His	Arg	Ala

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50	55	60													
Ile	Asn	Asp	Leu	Leu	Lys	Pro	Glu	Leu	Asp	Ala	Gly	Leu	His	Ala	Leu
65			70			75			80						
Ala	Val	Glu	Pro	Ala	Ala	Pro	Gly	Glu	Pro	Thr	Arg	Trp			
			85			90									

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: *cobu*
- (B) LOCATION: 2099-3115 bp of SEQ ID NO: 30
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATGAGTGCCA	CGGGCCTGCC	GTTTGATGAT	TTTCGCGAAT	TGTTGCGCAA	CCTGCCGGGC	60
CCGGATGCGG	CAGCCCTCGT	TGCGCGCGG	GAGCGGGACG	CCCAGCTGAC	GAAGCCGCCG	120
GGCGCGCTCG	GCCGCCCTGA	GGAAATGCC	TTCTGGCTCG	CCGCCCTGGAC	GGGCAAGGCG	180
CCGGTGGTCA	ACCGGCCGCT	GGTGGCGATC	TTTGCCGGCA	ACACAGGCGT	CACCCGCCAG	240
GGGGTGACCC	CGTTCCCGTC	ATCCGTCAAC	GCACAGATGG	TCGAGAATT	TGCCGCCGGT	300
GGCGCTGCGA	TCAACCAGAT	CTGCGTCAGC	CACGACCTCG	GGCTGAAGGT	CTTCGACCTC	360
GCACTCGAAT	ACCCGACCGG	TGATATCACC	GAGGAAGCCG	CGCTGTCCGA	GCGCGATTGC	420
GCCGCGACCA	TGGCCTTTGG	CATGGAGGCG	ATTGCCGGCG	GCACGGATCT	TCTGTGCATC	480
GGCGAAATGG	GCATCGGCAA	CACCA CGATC	GC GGCGCGA	TCAATCTCGG	CCTTTATGGT	540
GGCACGGCCG	AAGAATGGGT	CGG TCCGGGT	ACC CGGCTCCG	AGGGCGAGGT	GCTGAAGCGC	600
AAGATCGCCG	CGGTCGAAA	GGCCGTGGCG	CTGCATCGCG	ATCACCTGTC	CGATCCGCTC	660
GAACTGATGC	GTCGCCCTCG	CGGTCTGTAG	ATCGCGGCCA	TGGCTGGCGC	CATCCTGGCC	720
GCCCCGCTCC	AGAAGGTACC	TGT CATCATC	GACGGCTACG	TGGCGACCGC	TGCGGCTTCG	780
ATCCTGAAGG	CGGCCAACCC	GTCGCCCTC	GACCA TTGCC	TGATCGGCCA	TGTTTCCGGC	840
GAACCGGGGC	ATCTGCGCGC	GATCGAGAAG	CTCGGCAAGA	CGCCGCTGCT	GGCACTCGGC	900
ATGCGGCTTG	GCGAAGGGAC	GGGCGCGGCC	CTTGCCGGCG	GTATCGTCAA	GGCGGCGGCC	960
GCTTGCCACA	GGGGCATGGC	GACCTTTGCC	CAGGCCGGCG	TCAGCAACAA	GGAATAG	1017

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBU
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Ser Ala Ser Gly Leu Pro Phe Asp Asp Phe Arg Glu Leu Leu Arg  
 1 5 10 15  
 Asn Leu Pro Gly Pro Asp Ala Ala Ala Leu Val Ala Ala Arg Glu Arg  
 20 25 30  
 Asp Ala Gln Leu Thr Lys Pro Pro Gly Ala Leu Gly Arg Leu Glu Glu  
 35 40 45  
 Ile Ala Phe Trp Leu Ala Ala Trp Thr Gly Lys Ala Pro Val Val Asn  
 50 55 60  
 Arg Pro Leu Val Ala Ile Phe Ala Gly Asn His Gly Val Thr Arg Gln  
 65 70 75 80  
 Gly Val Thr Pro Phe Pro Ser Ser Val Thr Ala Gln Met Val Glu Asn  
 85 90 95  
 Phe Ala Ala Gly Gly Ala Ala Ile Asn Gln Ile Cys Val Ser His Asp  
 100 105 110  
 Leu Gly Leu Lys Val Phe Asp Leu Ala Leu Glu Tyr Pro Thr Gly Asp  
 115 120 125  
 Ile Thr Glu Glu Ala Ala Leu Ser Glu Arg Asp Cys Ala Ala Thr Met  
 130 135 140  
 Ala Phe Gly Met Glu Ala Ile Ala Gly Gly Thr Asp Leu Leu Cys Ile  
 145 150 155 160  
 Gly Glu Met Gly Ile Gly Asn Thr Thr Ile Ala Ala Ala Ile Asn Leu  
 165 170 175  
 Gly Leu Tyr Gly Gly Thr Ala Glu Glu Trp Val Gly Pro Gly Thr Gly  
 180 185 190  
 Ser Glu Gly Glu Val Leu Lys Arg Lys Ile Ala Ala Val Glu Lys Ala  
 195 200 205  
 Val Ala Leu His Arg Asp His Leu Ser Asp Pro Leu Glu Leu Met Arg  
 210 215 220  
 Arg Leu Gly Gly Arg Glu Ile Ala Ala Met Ala Gly Ala Ile Leu Ala  
 225 230 235 240  
 Ala Arg Val Gln Lys Val Pro Val Ile Ile Asp Gly Tyr Val Ala Thr  
 245 250 255  
 Ala Ala Ala Ser Ile Leu Lys Ala Ala Asn Pro Ser Ala Leu Asp His  
 260 265 270  
 Cys Leu Ile Gly His Val Ser Gly Glu Pro Gly His Leu Arg Ala Ile  
 275 280 285  
 Glu Lys Leu Gly Lys Thr Pro Leu Leu Ala Leu Gly Met Arg Leu Gly  
 290 295 300

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Glu Gly Thr Gly Ala Ala Leu Ala Ala Gly Ile Val Lys Ala Ala Ala  
 305 310 315 320  
 Ala Cys His Ser Gly Met Ala Thr Phe Ala Gln Ala Gly Val Ser Asn  
 325 330 335  
 Lys Glu

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 909 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: Pseudomonas denitrificans
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: cobV
  - (B) LOCATION: 1885-2793 bp of SEQ ID NO:30
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATGAAAGGTC	TGGGAAAAGT	GTGCGCGGCC	CTCGCGGGTG	CGCCCGCCCCG	GCTTGCAGAGA	60
CTCGCCGCAG	TCGGCGAGTT	TGGCAGCGGC	CGGGTCAATG	GCCGCAACCT	TGGAGGAGCC	120
ATGGGCTTCG	TTGGCGATTG	CTGTGACGAT	GTGGCGCGGT	CGATCGGCTT	TCTCAGCCGC	180
ATCCCAGATGC	CTGCGCGTCA	TTTCAAGGTT	TATGACGGGC	GCTTGAGCCG	TGCCGTGCGC	240
GCCTTCCCGT	TCGCCGGCCT	GGCGATCGCA	CTGCCATCGG	CGGCCGTCGC	CATGCCCTC	300
ATGGCGCTGC	AGGTGAGCTC	GCTCTTGCC	GCCTTTGTCG	TCGTGCCAT	CCAGGCGCTT	360
GTCACCGGCG	CACTGCACGA	AGACGGGCTT	GGCGACACGG	CCGATGGCTT	TGGCGGGGTT	420
CGCGACCGCG	AAGCGGCCT	TGCGATCATG	AAGGACAGCC	GCATCGGCAC	CTATGCGGCC	480
GTCGCCCTCA	TCCTCTCCTT	CGGCCCTGCGC	GTCTCGGCGT	TCGCCCTCGAT	CCTGCCGCTC	540
TTTCGCGCGC	TGGGCGCCGC	CATGGCGATC	CTTGGCGCAG	CGTGCCTCAG	CCGCGCCGCC	600
ATGGTCTGGC	ACTGGTCGTC	GCTTCCGCCG	CGCGCGACGA	CGCGCGTCGC	GGCCTCGGCT	660
GGCGAGCCGG	AACCGCGGC	CACCGCCTTC	GCGCTTGCGCT	TCGGAATTCT	TGTCGCAATG	720
CTGCTTTCT	ATCTCGCGCA	GGTCCCAGCG	CTCGCGTCA	TCGCGCGCT	CGTCGCATTC	780
CTTGCACGG	TCAAGGGCTT	CGCTCGGCTG	CGCATGCGCA	AGATCGGCGG	ACAAACGGGC	840
GACACGATCG	GGGCGACGCA	GCAACTGACCC	GAAATCGCCG	TGCTCGGTGC	CCTTGCCTG	900
ACGGTTTGA						909

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 302 amino acids
  - (B) TYPE: Amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBV
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Lys Gly Leu Gly Lys Val Cys Ala Ala Leu Ala Gly Ala Pro Ala  
1 5 10 15  
Arg Leu Ala Arg Leu Ala Ala Val Gly Glu Phe Gly Ser Gly Arg Val  
20 25 30  
Asn Gly Arg Asn Leu Gly Gly Ala Met Gly Phe Val Gly Asp Phe Cys  
35 40 45  
Asp Asp Val Ala Arg Ser Ile Gly Phe Leu Ser Arg Ile Pro Met Pro  
50 55 60  
Ala Arg His Phe Glu Gly Tyr Asp Gly Arg Leu Ser Arg Ala Val Arg  
65 70 75 80  
Ala Phe Pro Phe Ala Gly Leu Ala Ile Ala Leu Pro Ser Ala Ala Val  
85 90 95  
Ala Met Ala Leu Met Ala Leu Gln Val Ser Ser Leu Phe Ala Ala Phe  
100 105 110  
Val Val Val Ala Ile Gln Ala Leu Val Thr Gly Ala Leu His Glu Asp  
115 120 125  
Gly Leu Gly Asp Thr Ala Asp Gly Phe Gly Gly Arg Asp Arg Glu  
130 135 140  
Ala Ala Leu Ala Ile Met Lys Asp Ser Arg Ile Gly Thr Tyr Ala Ala  
145 150 155 160  
Val Ala Leu Ile Leu Ser Phe Gly Leu Arg Val Ser Ala Phe Ala Ser  
165 170 175  
Ile Leu Pro Leu Phe Ser Pro Leu Gly Ala Ala Met Ala Ile Leu Gly  
180 185 190  
Ala Ala Cys Leu Ser Arg Ala Ala Met Val Trp His Trp Ser Ser Leu  
195 200 205  
Pro Pro Ala Arg Ser Ser Gly Val Ala Ala Ser Ala Gly Glu Pro Glu  
210 215 220  
Pro Ala Ala Thr Arg Phe Ala Leu Ala Phe Gly Leu Leu Val Ala Met  
225 230 235 240  
Leu Leu Phe Tyr Leu Ala Gln Val Pro Ala Leu Gly Val Ile Ala Ala  
245 250 255  
Leu Val Ala Phe Leu Ala Thr Val Lys Gly Phe Ala Arg Leu Ala Met  
260 265 270  
Arg Lys Ile Gly Gly Gln Thr Gly Asp Thr Ile Gly Ala Thr Gln Gln  
275 280 285  
Leu Thr Glu Ile Ala Val Leu Gly Ala Leu Ala Leu Thr Val  
290 295 300

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13144 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: No

## (iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

## (ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Nucleotide Sequence of the 5' to 3'

strand from the 13144 bp SstI-SstI-SstI-SstI-BglII-BglII fragment of *Pseudomonas denitrificans*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGCTCGAAG	GGGCTTCCGC	CCCGATCGCT	GGCGTTAGCC	GACGTTCGAC	GTGCGGATGA	60
CGCCGAGCGG	GGCGAAGGGC	GCGTCGACGA	CGAGGTTGCG	TACCGCGCAG	TGGCTGGACG	120
GAACCTTCGA	GTTCCAGGGC	ATCTGAACGA	AATTGGGCTT	GCTGAAAATA	TACAGCATGG	180
ACATGAACCT	TGAGAGGCCG	GAGGCCCTATC	CTCCGGGGCG	TGTTGCTATG	CCGCTGATAT	240
AGGTGTGCGC	TGCAAAAAAT	TGAATGCCAA	ACTCGCCACG	CCATGTCGCA	TTCTGGTAT	300
CGGCCGCGAC	ATTTTCGACA	AGCCTTGCAGA	AAGCGCGAAA	CAATGCGTGA	AAGGGCTTTG	360
TCAATTGCGG	CGAAATCGTG	TCGAAACAGA	CCTTTGCCGC	TGCCCCTTTG	AGTGTACCG	420
ATGGCCGCAT	GACACGCAAG	ATCATGTTGC	AGGGAACCGG	CTCGGATGTC	GGAAAATCGG	480
TATTGGTGGC	GGGGCTCTGC	CGGCTTCCGC	CCAATCAGGG	CCTGAAGGTC	CGGCCGTTCA	540
AGCCGCAGAA	CATGTCGAAC	AACGCCGCCG	TTTCCGACGA	CGGGCGCGAG	ATCGGCCGCG	600
CGCAATGGCT	GCAGGCGCTG	GCCGGCGCG	TGCCGTCGTC	GGTGCACATG	AACCCGGTGC	660
TCCTGAAGCC	GCAGTCGGAC	GTGGGCAGCC	AGATGTCGTC	TCAGGGCAAG	GTCGCCGGGC	720
AGGCCAGGGG	GGGGGAATAT	CAGGGCCTCA	AGCCAAGCT	GCTGGGCGCC	GTCATGGAGA	780
GTTTGAACA	AATATCGGCC	GGTGGCGATC	TCGTGGTGGT	CGAAGGCGCC	GGCTCGCCGG	840
CCGAATCAA	CCTCAGGCC	GGCGACATCG	CCAATATGGG	CTTTGCGACA	CGGGCCAATG	900
TGCCGTCGT	GCTGGTCGGC	GACATCGACC	GGGGGGGGGT	GATCGCCTCG	CTGGTCGGCA	960
CGCATGCGAT	CCTGCCCAG	GAAGACCGGC	GCATGGTGAC	CGGCTATCTC	ATCAACAAGT	1020
TCCGCGCGA	CGTCACGCTG	TTCGACGACG	GCATTGCTG	CGTCAACCGC	TACACCGGCT	1080
GGCCCTGCTT	CGGCGTCGTG	CCGTGGCTGA	AGGCGGCGGC	ACGGCTGCCG	GCGGAAGATT	1140
CCGTCGTGCT	GGAGAAAGCTG	ACGCGCGGCCG	AGGGCGGGGC	GCTGAAGGTT	GCCGTCCCGG	1200
TACTGTCGCG	CATCGCCAAT	TTCGACGACC	TCGATCCGCT	CGCCGCCGAA	CCGGAGATTG	1260
ATCTCGTCTT	CGTGCGGCCT	GGCAGTCCCA	TTCCGGTCGA	CGCTGGCCTC	GTCGTCAATT	1320
CCGGGTCGAA	ATCGACCATC	GGCGACCTCA	TCGATTTCCG	TGCGCAAGGG	TGGGACCGTG	1380
ACCTCGAACG	TCATGTCGGC	CGGGCGGCCG	GGGTCATCGG	CATCTGCGGC	GGCTACCGAGA	1440
TGCTCGGCCG	GGCGCGTCACC	GATCCGCTCG	GCATCGAGGG	CGCGAACGT	GCGGTGAGG	1500
GCCTCGGGCT	GCTCGAGGTC	GAGACCGAGA	TGGCGCCGGA	AAAGACGGTG	CGAACACAGCC	1560
GCGCTGGTC	GCTGGAGCAT	GATGTGGTGC	TCGAAGGCTA	CGAAATCCAT	CTTGGCAAGA	1620
CGCAAGGTGC	GGACTGTGGC	CGGCCGTCGG	TGCGCATCGA	CAATCGCGCC	GACGGCGCCC	1680

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TTTCGGCCGA	TGGCCGCGTG	ATGGGCACCT	ACCTGCATGG	GCTCTTCACC	AGCGACGCC	1740
ATCGCGGCCG	GCTGCTCAAG	AGTTTCGGCA	TCGAAGGCCG	CGCCAACAAAC	TACCGCCAAT	1800
CGGTGATGC	GGCGCTCGAC	GATGTCGCGA	ACGAACCTGGA	GGCTGTGCTC	GATCGTCGCT	1860
GGCTGGACGA	GTTGCTCAGG	CACTAGGGAC	GGGGCAACGG	TCAGCCAGCA	GGTCGGTAC	1920
GTCGGGCCA	ACAGGAGCAA	CGAGCTTATC	CGACGGAAC	ACGCTGCGAC	ATCGTGTCTC	1980
TCGTTGCGG	CTTCCCAGAC	TTCCCGCGCG	GCATCCAGGT	TCATCAGGGC	AATCCCAGG	2040
CCGACGATCA	GGTCCGGCCA	GGCCGACTGC	CACAGATAGG	CTGTGCCCC	ACCCGCGGCG	2100
ATGATGGCCA	CATTGGCGAA	GGCATCGTTG	GGGGCCGAGA	GAAATGCTGC	CCGCGTGAGC	2160
GTGCCGCTCG	TGTGACGGTA	GGCGACGAGC	AGATAGGGCG	AGAAAGAGGT	GACCACCAAG	2220
GCCCCAAGTC	CGGTCAAGGA	CAGGGCAAAG	GGCTCTGGCG	GGACCGGATC	CATGAACCTC	2280
GCCCCAGGCCG	TCCAAAGGAA	GGCCAGCGCC	GGTACCAAGTA	GAATGAACGC	CATGCCATG	2340
CCGACCCGCG	CGCGGGTTCG	CGCCGTCCAG	GCCAGAGCAA	AGAAAATCAG	CATGTTGACG	2400
GAGGCCTCTT	CGAGGAAGTC	GACGCTGTCG	GCCATGAGGG	ACACCGAGCC	GATCGAAAGC	2460
GCGACAAGGA	GTTCGACCCC	GAAATAGCCA	AGGTTCAACA	GGGAGACGAT	GAGGACGACG	2520
CGGCGCAGGT	CGGTATCCAC	TCGAAAGGTT	CCCTTCTGG	CGAGATTGCG	CCTCGGACT	2580
TTTTTTGGCG	AGATTGCGCC	TCGGCACTTT	GGCACAGGTG	TTAGCAGCAG	TTTGTATCC	2640
ATAGCACTAG	GTTCGACAT	CGGTTCCGTT	CACACTGCCG	TCGTGCTGA	CGCCCGACAA	2700
ATCGTCGCGT	GGCGCAACTC	GGCCGGGGAG	GCGTCGATG	CGTCGATTGA	CTTGGGCTG	2760
CCCGCTTCCT	AATCATCAGG	TGTTGGATGG	TTCCCCCTTG	TCGTGGCGAT	CTGGGGGAAT	2820
AATTGGAAT	GTGACGGATG	GACCCAAATC	GGGCATCCTT	ATCGCAGCCG	ACCCCGCGAC	2880
TGAGAACCGG	TCAGGGTTCG	CCATCGGGAT	TGGTCCGGG	CTGTGGCCCG	GTTGATGGG	2940
CAATCGGGGC	AGGTGGGGGA	TCAAGCCGGA	AAAGGCACTG	GCGTGGCATC	GTGATCAGCC	3000
GGGTTGGAC	GCCTCTTCTT	CTAGAAATCG	TCCGCCCTTC	ACGATGTCCC	TCACAGCGCC	3060
CATCGCTCGG	AGACGACGCG	CAAAGGTTCG	CTGTGGCACC	GGAAAGACGC	CGGGAAGGTG	3120
AGGCGGCCG	CTCGGGCCT	GACATCGGAA	CCTTGCCGT	TAAGGGCGAG	GCGATGTTCG	3180
GCCCCGTACG	CCGTGAGC	GGAGACCTGC	CATCCGGCAT	GGGCATTCCG	CCCGAGGGGA	3240
CTTTTGCTC	CAACGCCATC	ACGGAGGTTG	TTTGGCTG	CAGATGTTT	CAAGAACCGG	3300
CCCGTGGCGC	GTCCGATGGC	TTTGCCACC	GACGGCTGAT	TTGGAATGT	TGAGGCAGCC	3360
ACGATGAGCA	GTCTCAGCGC	CGGGCCCGTG	CTGGTCCTTG	GCGGCGCCCG	TTCCGGCAAG	3420
TCCAGCTTT	CCGAGAGGCT	CGTCGAAGCG	TCCGGCTTCA	CCATGCATTA	TGTCGCCACG	3480
GGCCGCGCCT	GGGACGACGA	AATGCGCGAG	CGCATCGACC	ATCACCGAC	GCGCCGCGC	3540
GAGGGCTGGA	CGACGCGATGA	GGAGCCGCTC	GATCTCGTCG	GCATCCTCAG	ACGCATCGAT	3600
GATCCCAAGCC	ATGTGGTCCT	GATGCACTGC	CTGACGCTAT	GGGTCAACAA	TCTCATGCTG	3660
GAAGAGCGCG	ACATGACGCG	GGAGTTGCGC	GCCCTTGTG	CGTATCTGCC	CGAGGCGCGG	3720
GCGCGCCTCG	TCTTGTTC	CAATGAGGTC	GGCCTCGCA	TCGTGCCGA	GAACCGCATG	3780
GCCCGCGAGT	TTCGCGACCA	TGCGGCCCGG	CTTCACCAAGA	TCGTTGCGGA	GAAATCCGCT	3840
GAAGTTTACT	TTGTCGCGGC	CGGTTTCCG	CTGAAAATGA	AGGGTTGATC	CATGACCACT	3900
GCGAGAGCCA	ACCAGGGCAA	GATCCCGGCG	ACCGTCATCA	CCGGCTTCC	CGGCGCCGG	3960
AAGACGACGA	TGATCGCAA	CCTCTGCGAG	AACGCCGACG	GCAAGCGAT	CGGCTGATC	4020
ATCAACGAGT	TCGGCGATCT	TGGCGTCGAC	GGCGATGTCT	TGAAGGGCTG	CGGTGCCGAG	4080
GCCTGCACCG	AGGACGACAT	CATCGAGCTC	ACCAATGGCT	GCATCTGCTG	CACCGTGGCT	4140
GACGATTTCA	TCCCAGCCAT	GACGAAGCTG	CTCGAGCGTG	AAAACCGTCC	TGACCAACATC	4200
ATCATCGAAA	CCTCGGGCCT	TGCCCCGCG	CAGCCGCTGA	TCGCCGCTT	CAACTGCCG	4260
GATATCCGCA	GCGAAGTGAC	CGTCGATGGC	GTCGTCACCG	TGGTCACAG	CGCCGCCGTT	4320
GCCGCTGGCC	GCTTGTCCGA	CGACCAACGAC	AAAGGTCGATG	CGCTGCGCGT	CGAGGACGAC	4380
AATCTCGATC	ACGAAAGGCC	GATGAGGAG	CTGTTCGAGG	ATCAACTGAC	GGCTGCCGAT	4440
CTCATCGTT	TCAACAAGAC	CGATCTGATC	GATGCCCTCG	GCCTCAAGGC	CGTGCACGAC	4500
GAGGTGTCTT	CGCGCACCAAG	CCGCAAGCCC	ACGATGATCG	AGGGAAAAAA	CGGCGAAGTC	4560
GCCGCTGCCA	TCCTGCTTGG	CCTCGGTGTC	GGCACGGAAA	GCGATATCGC	CAACCGCAAG	4620
TCGCATCACG	AGATGGAGCA	CGAGGCAGGT	GAGGAGCAGC	ATCACGACGA	GTTCGACAGC	4680
TTCGTCGTCG	AGCTCGGTT	GATGCCGAT	CCGGCCGCT	TCATCGATCG	CCTGAAGGGC	4740
GTAATCGCG	AGCACGACGT	TCTGCGCTC	AAGGGTTTG	CAGACGTGCC	CGGCAAGCCG	4800
ATGCGCTCC	TGATCCAGGC	GGTCGGCGCC	CGCATCGACC	AATATTACGA	CCGCGCTTGG	4860
GGCGCTGGCG	AAAAGCGCGG	TACGCGCTC	GTCGTCATCG	GCCTGACGA	CATGGACGAG	4920
GCGGCGGTGC	GCGCCGCGAT	CACCGCGCTC	GTGTAGATCG	TTCTTGTAA	GAAATGATCT	4980
AACGCATTGA	AATGATGCA	TTCCGGATGG	AGAACGCTTT	TAGCGTTTC	GTTCGGAATT	5040
GCCCCAACGG	ACAAGACGAA	TGCATCTGCT	TCTCGCCCG	AAAGGAACGA	TCGCCCACGG	5100
CAACGAGGCG	ATCGACCTTG	GGCAAAACGCC	GGCCGATATC	CTTTTCCAT	CGGCGCCCGA	5160
CACCGAGCTC	TCCTCGATCG	CCGCGGCTCA	CGGCCGACGC	GACGGAGGCT	TGAGCCTGCG	5220
CATGCCAGC	CTGATGAGCC	TGATGACCC	GATGTCGGTC	GACACTTACG	TCGAGCGCAC	5280
GGCGCGTCAC	GCCAAGCTGA	TCGTCGTCG	GGCGCTCGGT	GGGCCAGCT	ATTTCCGTTA	5340
TCTGCTGGAA	GCCCTGATG	CGGCTGCCGT	CACCCATCGT	TTCGAGATCG	CGGTTCTGCC	5400
GGGTGACGAC	AAGCCGGATC	CGGGGCTGGA	GCCTTCTCC	ACCGTCGAG	CCGACGACCG	5460

CCAGGCCCTT	TGGGCTTA	TCACCGAAGG	CGGCTCGAC	AATGCCGGGC	TGTTTCTCGA	5520
CTATGCCGCC	GCACTGGTCA	CAGGTGCGGA	GAAGCCGAG	CCGGCAAAGC	CCCTGTTGAA	5580
GGCCGGCATC	TGGTGGCCGG	GTGCTGGTGT	GATCGGCGTC	AGCGAATGGC	AGTCCCTTGT	5640
TCAGGGACGG	ATGGTAGCGA	GGGAGGGATT	CGAACCCCCG	ACGGTCGGGA	TCTGCTTTA	5700
CCGCGCGCTC	GTGAGAGTG	GCGAGACACG	GCCTGTGGAG	GCGCTGATCG	ATGCGCTGGA	5760
GGCTGAAGGT	GTGCGGGCAC	TGCGCGTGT	TGTCTCAAGC	CTCAAGGATG	CCGTTCCGT	5820
CGGCACGCTG	CAGGGATT	TTTCCGAGGC	CGCACCCGAC	GTGGTGTGAA	ACGCCACTGG	5880
CTTTGCCGTC	TCGTCGCCG	GTGCCGACCG	TCAGCCGACG	GTGCTGGAA	CGACCGGTGC	5940
GCCGGTGCTG	CAGGTGATT	TCTCCGGCTC	GTCGCGGGCG	CAATGGGAAA	CGTCGCCGCA	6000
GGGGCTGATG	GCGCGCGACC	TCGCCATGAA	CGTGGCACTC	CCCGAAGTCG	ATGGCCGAT	6060
CCTTGCAGCGC	GCCGCTCTCCT	TCAAGGCCGC	GTCGATCTAT	GACGCCAAGG	TGGAGGCCAA	6120
TATCGTCGGC	CATGAGCCGC	TCGAAGGCCG	GGTGCCTT	GCCGCTGATC	TTGCCGTCAA	6180
CTGGGCGAAC	GTGCGCCGGG	CAGAGCCCAC	CGAGCGCCTG	ATTGCCATCG	TCATGGCCAA	6240
CTATCGAAC	CGCGACGGTC	GCCTCGGAA	CGGTGTGGG	CTCGACACGC	CGGCCGGTAC	6300
CGTCGAGGTG	CTTAGCGCA	TGGCGCGGG	AGGCTATGCG	GTCGGTGAGG	TTCCCGCCGA	6360
TGGCAGCGC	CTGATCCGCT	TTCTGATGGC	CGGGCCGAC	AATGCGGCGA	GCCATGACCG	6420
TGAAATCCGC	GAGCGTATT	CGCTGAACGA	TTACAAAAGC	TTCTTCGATT	CGCTTCCGAA	6480
ACAGATAAAAG	GATGAAGTTG	CCGGTCGCTG	GGGCGTGGCG	GAGGCCGATC	CCTTTTCCCT	6540
CGATGGCGCC	TTCGCGCTGC	CGCTCGCCG	CTTCGGCAGG	GTGATCGTCG	GCATCCAACC	6600
GGCGCGCGGC	TACAAACATCG	ATCCGAAGGA	AAGCTACCAT	TCCCCGGACC	TCGTGCCGCC	6660
GCATGGCTAT	CTCGCCTTCT	ACGCCCTTCT	GCGCCAGCAG	TCGGAGCGC	AGGCAGATCGT	6720
CCACATGGGC	AAGCACGGCA	ATCTCGAATG	GCTGCCGGG	AAGCGCTGG	CGCTGTCGGA	6780
AACCTGCTAT	CCCAGCGA	TCTTCGGGCC	GCTGCCGAC	ATCTATCCCT	TCATCGTCAA	6840
CGATCCGGC	GAAGGTACCG	AGGCCAAGCG	CCGCACCAAGC	GCCGTATCA	TCGACCAACCT	6900
GACCCGCCCC	TTGACGCGC	CCGAATCTA	CGGCCCCGTC	AAGGATCTGG	AAGCGCTCGT	6960
CGACGAATAT	TACGACGCGC	CCGGCGGTGA	TCCGCGCCG	CTCAGGCTGC	TCAGCCGCCA	7020
GATCCTCGAT	CTCGTGCCTG	ACATCGGCCT	CGACAGCGAC	GCAGGCATCG	ACAGGGCGA	7080
CAGCGACGAC	AAGGCGCTGG	AAAAGCTGA	CGCCTATCTC	TGCGACCTCA	AGGAAATGCA	7140
GATCCGCGAC	GGCCTGCACA	TCTTCGGCGT	TGCGCCGAA	GGGCGGTTGT	TGACGGACCT	7200
CACCGTAGCG	CTGGCGCGC	TGCCCCGAGG	TCTCGCGAG	GGCGCGCACC	AGAGCCTGCA	7260
GCGGGCGATC	GCAGCGGATG	CGGGGCTGCG	TGGGTTGCT	ATTCCCACCT	CGGCGGGGG	7320
CAACCCCGCA	CGCGACGCC	AACCCTCGA	CCCGCTCGAC	TGCGTCATGT	CCGACACCTG	7380
GACAGGCCG	AAACCGTCCA	TCCTCGCTGA	CCTCTCGAC	GCCCCCTGGC	GCACCGCCGG	7440
CGATACGGTC	GAGCGCATCG	AGTTGCTTGC	CGCAAATCTC	GTGCGGGTG	AACTGGCTTG	7500
CCCGGACAC	TGGGCCAAC	CCCGCGCCGT	GCTCGGCGAA	ATCGAAACGC	GCCTGAAGCC	7560
GTCGATTCA	AACTCGGGTG	CCGCGAGAT	GACCGGCTTC	CTCACCGGTC	TCAGCGGCCG	7620
CTTCGCGCC	CCCGGTCCAT	CGGGCGCGCC	GACCGCGCCG	CGGGCGGATG	TGTTGCGAC	7680
GGGGCGCAAT	TTCTACTCGG	TCGACAGCGC	CGCCGTGGCG	ACGCCGGCGG	CTTACGAGCT	7740
TGGCAAGAAA	TCCGGCGAGC	TTCTGATCCG	CCGCTACCTG	CAGGACCATG	GCGAATGGCC	7800
GTCCTCTT	GGCCTGACCG	CCTGGGGCAC	GGCGAACATG	CGCACCGGCG	GCGACGACAT	7860
CGCCCAGGCC	CTGGCGCTGA	TCGGCGCCAA	GCCCACCTGG	GACATGGTCT	CTCGCCGGGT	7920
GATGGGCTAC	GAGATCGTC	CGCTCGCAGT	CCTCGCCCG	CCACCGCTCG	ACGTGACCTT	7980
GCGCATTTCC	GGCTTCTTCC	GCGATGCCCT	CCCAGCACCG	ATCGCGCTCT	TCGACAAGGC	8040
GATCCGCGCC	GTGCGCTGG	AGGAAGACGA	TGCGAACAC	ATGATCGCCG	CACGCATGCG	8100
GGCGGAAAGC	CGGCGGCTGG	AGGCCGAAGG	CGTGGAAAGC	GCCGAGGCCG	CGCGTCGCGC	8160
CTCCTACCGC	GTCTTTGGCG	CAAAGCCCAG	TGCTATGGC	GCCGCCCTGC	AGGCCTGTAT	8220
CGACGAGAAG	GGCTGGGAAA	CCAAAGCAGA	TCTCGCCAG	GCCTATCTTA	CCTGGGGCGC	8280
CTATGCCAT	GGCGCCGGCG	AGGAGGGCAA	GGCGGAGGC	GATCTTTCG	AGGAGGCCCT	8340
GCGCACGATA	GAGGCGGTGG	TGCAGAACCA	GGACAACCGC	GAGCACGATC	TGCTCGACAG	8400
CGACGACTAC	TACCACTTCG	AAGGCCGCAT	GAGCGCTGCC	GCCGAACAGC	TCGGCGTCA	8460
CCGTCGGCG	ATCTACCACA	ACGACCATTG	CCGTCCGAA	AAGCCTGTGA	TCCGGTCGCT	8520
CGAAGAAGAG	ATCGGCCGCG	TGGTCCGGGC	CCGCGTCGTC	AATCCCAAGT	GGATCGATGG	8580
CGTCATGCGC	CACGGATA	AGGGCGCTT	CGAGATCGCT	GCCACGGTCG	ACTACATGTT	8640
CGCCTTGCC	GCGACCACCG	GTGCGGTGCG	CGACCATCAT	TTGAGGCCG	CTTATCAGGC	8700
GTTCATGTC	GACGAGCGCG	TGGCTGACTT	CATGCGCGAC	AAGAACCCGG	CCGCTTTGC	8760
CGAGCTTGCC	GAACGCCCTG	TTGAAGCAAT	CGACCGCAAT	CTCTGGACGC	CGCGCTCGAA	8820
TTCGGCGCGG	TTTGAACCTT	CCGGCATCGG	CACGGCAGCA	ACCCGGCTTC	GTGCCGGCAA	8880
TGAATAGAGC	GGTTCGGGGC	TGGCGGTTAT	CCGTCCGAA	TTGCTGGAA	ACAAAGACCT	8940
GGTTCCGTTT	CGCTGCTCAG	TGAAGTGCAG	AAAGGAACCG	AAGCGGGACG	AGGGCGTCTG	9000
CCCATCCCGA	ACTTGAGAAC	TGAGGGAGTG	ATCATGAGCG	ACGAGACGAC	AGTAGGGCGC	9060
GAAGCCCCGG	CCGAGAAGGA	CGATGCCGC	CACGCCATGA	AGATGGCGAA	GAAGAAGGCA	9120
GCACCGAAGAA	AGATCATGGC	GACGAAGACC	GACGAGAAGG	GTCTGATCAT	CGTCAACACC	9180
GGCAAAGGCA	AGGGCAAGTC	GACCGCCGGC	TTCGGCATGA	TCTCCGCCA	TATCGCCAC	9240

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GGCATGCCCT	GCGCCGCTGT	GCAGTTCATC	AAGGGTGC GA	TGGCAACCGG	CGAGCGCGAG	9300
TTGATCGAGA	AGCATTTCGG	CGATGTCCTGC	CAGTTCTACA	CGCTCGGC GA	GGGCTTCACC	9360
TGGGAAACGC	AGGATCGCGC	CCGCGATGTT	GCGATGGCTG	AAAAGGCCTG	GGAGAAGGCG	9420
AAGGAACCTGA	TCCGTGACGA	GCGCAACTCG	ATGGTCTGC	TCGACGAGAT	CAACATTGCT	9480
CTGCCTACG	ACTACATCGA	CGTCGCCGA A	GTGGTGCCTG	TCCTGAAGGA	AGAAAAGCCG	9540
CACATGACGC	ATGTGGTGT	CACCGGCCGC	AACCGCAAGA	AAGACCTGAT	CGAAGTCGCC	9600
GATCTCGTCA	CTGAGATGGA	GCTGATCAAG	CATCCGTTCC	GTTCCGGCAT	CAAGGCGCAG	9660
CAGGGCGTGG	AGTTCTGTG	AGCCAGAGCT	GGCAGTTCTG	GGCGCTGCTT	TCGGCCGCCT	9720
TCGCTGCCT	CACGGCGGTG	TTTGCCAAGG	TCGGGGTTGC	GCAGATCAAC	TCCGACTTCG	9780
CAACGCTGAT	CCGCACCGTC	GTCATCCTCT	CGTGATCGC	CGCCATCGT	GCGGCGACAG	9840
GGCAGTGGCA	GAAGGCCATCG	GAAATCCC GG	GCCGCACCTG	GCTGTTCTG	GCGCTGTCAG	9900
GGCTTGCAC	TGGCGCTTCC	TGGCTTGCCT	ATTTCCGCGC	GCTGAAGCTC	GGCGACGCCG	9960
CCCGCGTGGC	GGCGCTCGAC	AAGCTCTCGA	TCGTATGGT	CGCGATCTTC	GGCGTGTCTCT	10020
TCCTCGGTGA	AAAGCTCAAC	CTGATGAACT	GGCTCGGCGT	CGCCTTCATT	GCGCCGGGGG	10080
CGCTGTTGCT	GGCGGTGTTT	TGAGCGCGCC	TGCTCTGGT	CCTGTTCACT	GAATGCTCGC	10140
CTCAATCAAT	CGTAATCCC	GACACATGCA	GTGGTTGTGA	CGAGCGGGAG	GACGGCATGC	10200
AGATTGAAGG	CAATTGGAGC	GAGGCCCTTC	CTGATCCGTC	GGGCCACGTC	GCGCAGTTCG	10260
GCAGACGCTG	GAAGCGCTGC	AGCCTGAGGG	TGAGCCCTGC	TTCAGACCCA	CCGGCGGACA	10320
CGCCTGCAAT	AGGCACCGTA	GGCGTCGCCG	AAGACCTTGG	CGAGGTGGGT	TTCCTCCATG	10380
CGGATCTGGT	AGGAAATCTGA	GATCCAGGCG	GAGAGCGCCA	GCGGCCACCGA	GATGACGTTG	10440
GGCACCGCCA	TCACCGTGCC	GATCAGCGCG	GTCAACATGC	CGACATAGAT	CGGGTTGCGC	10500
GAGAAGGCAT	AGAGGCCCTGA	GGTCACAAGC	GGCGCGTCTC	GCTTTTCAGG	GATGCCGATC	10560
TTCCAGGAAT	GACGCATCGC	CCATTGCGAC	AGCATCGTC	GCCCCGCCGCC	GAGCGTCATC	10620
AGCGCAGGGC	CGACGGCGT	AAGGATGGGC	GTGTCAGCG	CCGGGATCCG	GCCGAGGGCA	10680
GCATCGACGG	AGGCCGGGAG	CATGGCGACC	GCCAGCAGGT	GGATCACCA	CGCTGCGACG	10740
ATCAGGCGGA	AAAGCCTGCC	CGCAAACCCCT	TCCGCATCGT	CGCCATAGGT	TAGCACGACC	10800
GGCGAGCGGC	CGGATTGCAC	GCGGCGGAGG	ATCGCCAGCG	CGAGCGTGG	CAATCCCACG	10860
ACGAGCATCA	GGATGGTGGG	AAGGGTGGTG	GACATGGAA	CCTCTGGAGC	GAGCTGACAA	10920
GACAGGAGCG	CACGACGGGT	AGGCGGCCA	TATGAGCGTC	TACCCGGCGA	AGCATTCTGA	10980
TCACCTTGCA	ATCTCTAGTA	ACTAGAGGTT	CAAGCTCGG	ACCTGTCCG	CTTCCTGCTG	11040
GGTTACCGGA	TCTTATTGCC	AAGCGTTGGA	GGCTGTCA	TCGCCCCCG	CCGTGTCGGA	11100
AGGTCCGCAA	AATTCTGCTC	TTGACGGCTG	CTCCTTCCTG	CGAGCGATTG	CATAGGCAGG	11160
AGGCCGCA	CATGTTAGAC	CGTCGACAGG	CTAAATACGG	GTGAAACCTG	AAGAATACTC	11220
TCAGAGCTGC	GGTTGGTGT	GCATCGGTCT	TGCTGTTCTT	GTGATCAGGT	GTGGCGGGC	11280
AGGCCAAC	CGTGAAGAGC	GGGGCGTCAC	GAGCTCAAGA	AACGACGACC	ACCCAGAAGG	11340
CGAACCGAA	AACTAAAACG	ACGCGCAAGC	AAAGGGCTGC	GGATGAAGCC	AAGGCCAAGG	11400
CGCTCGCCGA	AGCGCGCCGT	CCACGGGTTT	GCAAGAGCG	GGAGAGCGAA	TGCACTATG	11460
GCGCAGGTCC	GGTCGGAGAG	CAGTGTCTG	GCTGGTCGA	ATCCGGTGC	CCTGATCTG	11520
GCATAACTGT	CAGGCGTTGA	CCGCCCGCGA	CCTTCGCGC	GGCAGGCAAG	CGTGTGTCG	11580
TCGAAGCGAC	GCCTGACGCG	ATAGAAATCA	CGGGTCGCT	GGTTGTTCT	GAAGCTTGG	11640
GATTGGTTT	AGGTGATGGA	AGCCGGCGT	GAACGAAAA	TAATGATCGA	TCTCGAGAAC	11700
AGCGCGCTCC	AGTTTGCAAC	CCGAGCACAC	GGCGAACAGA	AGCGTAAGTA	TGACGGTCGG	11760
CCCTATATCG	TTCATCCGAT	TGCGGTGGCG	GAGATTGTT	GAAGCGTGC	CCATACGCC	11820
GAAATGATCG	CCGCAGCGCT	GCTTCACGAT	ACGGTCGAAG	ATACCGACGC	GACGCTGCTG	11880
GAGATCAAGG	AAGCGTTCGG	CCCCAAGGTC	GCAACACTGG	TTGCGTGGCT	CACCGACATA	11940
TCCACTCCGT	TCCACGGCAA	CCGACAGGTG	CGCAAGGAAC	TGGATCGCCA	GCACCTCGCA	12000
TCGGCGCCCG	CCGCGGGCGAA	AACCGTCAAG	CTCGCCGACC	TGATCGACAA	TGCGATAGCG	12060
ATCAAAGCCG	GGGATCCGAA	TTTCTGGAAA	GTGTTCGCG	CCGAGATGAA	ACGTTGCTG	12120
GAGGTCTTGG	GGGACGGCGA	CGAGACCTT	CTCGCAAAGG	CCCGTGCATT	AGCGCCGGAA	12180
TGAGAGTGCC	GGCGTTTATC	GGCAAGCATG	TCTGTGCT	GTGACCCCG	TCAACCGTC	12240
ATCCAAGATC	GCAGAACCGA	CATGCTTTCG	CGGTTTTGC	CGCCGGTGTG	GCCCAGCCAC	12300
GCCTCACAGG	CTGCGCGGTT	GGGGCGCTTA	GGACAGCGCA	GAATTGCG	ACCGCGCCGC	12360
GCCTCAATGC	CCCAGCCAGA	TCCGCAAGGG	ATGCGTCGGA	TCTGCGAGCA	GCGGATTCG	12420
GAGCGCGATC	GAGACGATGA	CGAGCAGCGG	CTTGATGATC	TTGGCGCCCT	TGGCCATGGC	12480
ATAGCGCGAG	CCGACCTGGG	CGCCGAGGAA	CTGGCCGAGG	CCCATCAACA	GGCCGACCTT	12540
CCAGAGAACG	GGCGCGAAGA	AGAGGAAGAC	GCGGAAGGCG	CCGACGTTGG	AGCCAAAGTT	12600
GAGGAACCTC	GTGTGCGCCG	TCGCCTTCAA	CACGCCGAAG	CCGGCGAGGG	TAACGAAGCC	12660
GAGCATGAAG	AACGAGCGG	TGCGGGGGCC	GAAGACGCCG	TCATAAAAGC	CGATTAGCGG	12720
CACCAAGTGC	AGCGTGAAGA	CGAAGGGGGT	GACGCGCTG	TGCTGGTC	CGTCGCCAT	12780
GTTCGGCTTC	AGGCCGAAT	AAAGCGCAAT	GGCGATCAGC	AGAAAGGGCA	GGATCGCCTT	12840
CAGCACGTCG	CCGGGAACGA	TGGTTGCGAG	CAGGGCGCCG	AGCACGGCG	CGGCGGCCGA	12900
CATCAGCGCC	ATCGGCAGCT	GCTCTTTCAG	GTTCACGTGG	CCGGCGCCGGG	CATAGGACAG	12960
CGTGGCCGAG	CCGGAGCCGA	ACAATCCCTG	CAGCTTGTG	GTGCCGAGCG	TCTGCAAGGG	13020

CGGGATGCC	GCAATGAGCA	TGGCCGGAAT	GGTGATCATG	CCACCGCCGC	CGGCGATCGA	10724598	13080
ATCGATGAAG	CCTCGATGA	AGGCAGCGAC	GAACAGGAAG	GCGAGCAGGT	GGAAGGCGAG		13140
ATCT							13144

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1458 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas denitrificans*
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: *cobQ*
  - (B) LOCATION: 429-1886 bp of SEQ ID NO:41
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

ATGACACGCA	GGATCATGTT	GCAGGGAAACC	GGCTCGGATG	TCGGAAAATC	GGTATTGGTG	60
GCAGGGCTCT	GCCGGCTTGC	CGCCAATCG	GGCCTGAAGG	TCCGGCCGTT	CAAGCCGAG	120
AACATGTCGA	ACAACGCCG	CGTTCCGAC	GACGGCGGCG	AGATCGGCCG	CGCGCAATGG	180
CTGCAGGCGC	TGGCCGCGCG	CGTGCCGTCG	TCGGTGACAC	TGAACCCGGT	GCTCTGAAG	240
CCGCAGTCGG	ACGTGGGAG	CCAGATCGTC	GTTCAGGGCA	AGGTGCGCGG	GCAGGCCAGG	300
GGGCAGGAAT	ATCAGGCCT	CAAGCCCAAG	CTGCTGGCG	CCGTCATGGA	GAGTTTCGAA	360
CAAATATCGG	CCGGTGCCGA	TCTCGTGGTG	GTCGAAGGCG	CCGGCTCGCC	GGCCGAAATC	420
AACCTCAGGC	CCGGCGACAT	CGCCAATATG	GGCTTGCGA	CACGGGCCAA	TGTGCCGGTC	480
GTGCTGGTCG	GGCACATCGA	CCGCGGGGGG	GTGATCGCCT	CGCTGGTCGG	CACGCATGCG	540
ATCCTGCCG	AGGAAGACCG	GCGCATGGTG	ACCGGCTATC	TCATCAACAA	GTTCCGCGGC	600
GACGTCACGC	TGTTCGACGA	CGGCATTGCT	GCCGTCAACC	GCTACACCGG	CTGGCCCTGC	660
TTCGGCGTCG	TCGGCGTGGCT	GAAGGCAGCG	GCACGCTGC	CGCGGAAAGA	TTCCGTCGTG	720
CTGGAGAACG	TGACGCGCGG	CGAGGGCGG	GCGCTGAAGG	TTGCCGTCCC	GGTACTGTCG	780
CGCATCGCCA	ATTTCGACGA	CCTCGATCCG	CTCGCCGCCG	AACCGGAGAT	TGATCTCGTC	840
TTCGTCGCGC	CTGGCAGTCC	CATTCGGTC	GACGCTGGCC	TCGTCGTAT	TCCCAGGTG	900
AAATCGACCA	TCGGCGACCT	CATCGATTTC	CGTGCAGAAG	GGTGGGACCG	TGACCTCGAA	960
CGTCATGTGC	GCCGGGGCGG	CCGGGTATC	GGCATCTGCG	GCGGCTACCA	GATGCTCGGC	1020
CGGCGCGTC	CCGATCCGCT	CGGCATCGAG	GGCGGCGAAC	GTGCGGTGAA	GGGCCTCGGG	1080
CTGCTCGAGG	TCGAGACCGA	GATGGCGCCG	GAAAAGACGG	TGCGCAACAG	CCGCGCTGG	1140
TCGCTGGAGC	ATGATGTGGT	GCTCGAAGGC	TACGAAATCC	ATCTTGGCAA	GACGCAAGGT	1200
CGGGACTGTG	GCCGGCCGTC	GGTGCATC	GACAATCGCG	CCGACGGCGC	CCTTCGGCC	1260
GATGGCCGCG	TGATGGGCAC	CTACCTGCAT	GGGCTCTTC	CCAGCGACGC	CTATCGCGC	1320
GCGCTGCTCA	AGAGTTTCGG	CATCGAAGGC	GGCGCCAACA	ACTACCGCCA	ATCGTCGAT	1380
CGGGCGCTCG	ACGATGTGCG	GAACGAACTG	GAGGCTGTG	TCGATCGTCG	CTGGCTGGAC	1440
GAGTTGCTCA	GGCACTAG					1458

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 485 amino acids  
 (B) TYPE: Amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
 (A) ORGANISM: Pseudomonas denitrificans  
 (B) STRAIN:  
 (C) INDIVIDUAL ISOLATE:  
 (D) DEVELOPMENTAL STAGE:  
 (E) HAPLOTYPE:  
 (F) TISSUE TYPE:  
 (G) CELL TYPE:  
 (H) CELL LINE:  
 (I) ORGANELLE:

(ix) FEATURE:  
 (A) NAME/KEY: COBQ  
 (B) LOCATION:  
 (C) IDENTIFICATION METHOD:  
 (D) OTHER INFORMATION: Translation product of SEQ ID NO:42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Met Thr Arg Arg Ile Met Leu Gln Gly Thr Gly Ser Asp Val Gly Lys  
 1 5 10 15  
 Ser Val Leu Val Ala Gly Leu Cys Arg Leu Ala Ala Asn Gln Gly Leu  
 20 25 30  
 Lys Val Arg Pro Phe Lys Pro Gln Asn Met Ser Asn Asn Ala Ala Val  
 35 40 45  
 Ser Asp Asp Gly Gly Glu Ile Gly Arg Ala Gln Trp Leu Gln Ala Leu  
 50 55 60  
 Ala Ala Arg Val Pro Ser Ser Val His Met Asn Pro Val Leu Leu Lys  
 65 70 75 80  
 Pro Gln Ser Asp Val Gly Ser Gln Ile Val Val Gln Gly Lys Val Ala  
 85 90 95  
 Gly Gln Ala Arg Gly Arg Glu Tyr Gln Ala Leu Lys Pro Lys Leu Leu  
 100 105 110  
 Gly Ala Val Met Glu Ser Phe Glu Gln Ile Ser Ala Gly Ala Asp Leu  
 115 120 125  
 Val Val Val Glu Gly Ala Gly Ser Pro Ala Glu Ile Asn Leu Arg Pro  
 130 135 140  
 Gly Asp Ile Ala Asn Met Gly Phe Ala Thr Arg Ala Asn Val Pro Val  
 145 150 155 160  
 Val Leu Val Gly Asp Ile Asp Arg Gly Gly Val Ile Ala Ser Leu Val  
 165 170 175  
 Gly Thr His Ala Ile Leu Pro Glu Glu Asp Arg Arg Met Val Thr Gly  
 180 185 190  
 Tyr Leu Ile Asn Lys Phe Arg Gly Asp Val Thr Leu Phe Asp Asp Gly  
 195 200 205  
 Ile Ala Ala Val Asn Arg Tyr Thr Gly Trp Pro Cys Phe Gly Val Val  
 210 215 220  
 Pro Trp Leu Lys Ala Ala Ala Arg Leu Pro Ala Glu Asp Ser Val Val  
 225 230 235 240  
 Leu Glu Lys Leu Thr Arg Gly Glu Gly Arg Ala Leu Lys Val Ala Val  
 245 250 255  
 Pro Val Leu Ser Arg Ile Ala Asn Phe Asp Asp Leu Asp Pro Leu Ala

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260	265	270
Ala Glu Pro Glu Ile Asp Leu Val Phe Val Arg Pro Gly Ser Pro Ile		
275 280 285		
Pro Val Asp Ala Gly Leu Val Val Ile Pro Gly Ser Lys Ser Thr Ile		
290 295 300		
Gly Asp Leu Ile Asp Phe Arg Ala Gln Gly Trp Asp Arg Asp Leu Glu		
305 310 315 320		
Arg His Val Arg Arg Gly Gly Arg Val Ile Gly Ile Cys Gly Gly Tyr		
325 330 335		
Gln Met Leu Gly Arg Arg Val Thr Asp Pro Leu Gly Ile Glu Gly Gly		
340 345 350		
Glu Arg Ala Val Glu Gly Leu Gly Leu Leu Glu Val Glu Thr Glu Met		
355 360 365		
Ala Pro Glu Lys Thr Val Arg Asn Ser Arg Ala Trp Ser Leu Glu His		
370 375 380		
Asp Val Val Leu Glu Gly Tyr Glu Ile His Leu Gly Lys Thr Gln Gly		
385 390 395 400		
Ala Asp Cys Gly Arg Pro Ser Val Arg Ile Asp Asn Arg Ala Asp Gly		
405 410 415		
Ala Leu Ser Ala Asp Gly Arg Val Met Gly Thr Tyr Leu His Gly Leu		
420 425 430		
Phe Thr Ser Asp Ala Tyr Arg Gly Ala Leu Leu Lys Ser Phe Gly Ile		
435 440 445		
Glu Gly Gly Ala Asn Asn Tyr Arg Gln Ser Val Asp Ala Ala Leu Asp		
450 455 460		
Asp Val Ala Asn Glu Leu Glu Ala Val Leu Asp Arg Arg Trp Leu Asp		
465 470 475 480		
Glu Leu Leu Arg His		
485		

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 525 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: Pseudomonas denitrificans
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: cobb
  - (B) LOCATION: 3364-3888 bp of SEQ ID NO:41
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ATGAGCAGTC	TCAGCGCCGG	GCCCGTGTG	GTCTTGGCG	GCGCCCGTTC	CGGCAAGTCC	60
AGCTTTCCG	AGAGGCTCGT	CGAACGTC	GGCTTCACCA	TGCATTATGT	CGCCACGGGC	120
CGCGCTGGG	ACGACGAAAT	GCGCGAGCGC	ATCGACCATC	ACCGGACGCG	CCGCGGCGAG	180
GGCTGGACGA	CGCATGAGGA	GCCGCTCGAT	CTCGTCGGCA	TCCTCAGACG	CATCGATGAT	240
CCCAGCCATG	TGGTCCTGAT	CGACTGCCTG	ACGCTATGGG	TCACCAATCT	CATGCTGGAA	300
GAGCGCGACA	TGACGGCGGA	GTTGCCGCC	CTTGTGCGT	ATCTGCCGA	GGCGCGGGCG	360
CGCCTCGTCT	TTGTTTCAA	TGAGGTCGGC	CTCGGCATCG	TGCCCGAGAA	CCGCATGGCC	420
CGCGAGTTTC	GCGACCATGC	CGGCCGGCTT	CACCAAGATCG	TTGCGGAGAA	ATCCGCTGAA	480
TTTACTTTG	TCGCGGCCGG	TTTGGCGCTG	AAAATGAAGG	GTTGA		525

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBP
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met	Ser	Ser	Leu	Ser	Ala	Gly	Pro	Val	Leu	Val	Leu	Gly	Gly	Ala	Arg
1				5					10			15			
Ser	Gly	Lys	Ser	Ser	Phe	Ser	Glu	Arg	Leu	Val	Glu	Ala	Ser	Gly	Phe
					20				25			30			
Thr	Met	His	Tyr	Val	Ala	Thr	Gly	Arg	Ala	Trp	Asp	Asp	Glu	Met	Arg
					35				40			45			
Glu	Arg	Ile	Asp	His	His	Arg	Thr	Arg	Arg	Gly	Glu	Gly	Trp	Thr	Thr
					50				55			60			
His	Glu	Glu	Pro	Leu	Asp	Leu	Val	Gly	Ile	Leu	Arg	Arg	Ile	Asp	Asp
				65					70			75			80
Pro	Ser	His	Val	Val	Leu	Ile	Asp	Cys	Leu	Thr	Leu	Trp	Val	Thr	Asn
					85				90			95			
Leu	Met	Leu	Glu	Glu	Arg	Asp	Met	Thr	Ala	Glu	Phe	Ala	Ala	Leu	Val
					100				105			110			
Ala	Tyr	Leu	Pro	Glu	Ala	Arg	Ala	Arg	Leu	Val	Phe	Val	Ser	Asn	Glu
					115				120			125			
Val	Gly	Leu	Gly	Ile	Val	Pro	Glu	Asn	Arg	Met	Ala	Arg	Glu	Phe	Arg
				130				135			140				
Asp	His	Ala	Gly	Arg	Leu	His	Gln	Ile	Val	Ala	Glu	Lys	Ser	Ala	Glu

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145	150	155	160										
Val	Tyr	Phe	Val	Ala	Ala	Gly	Leu	Pro	Leu	Lys	Met	Lys	Gly
				165					170				

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1065 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas denitrificans*
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY: *cobW*
  - (B) LOCATION: 3892-4956 bp of SEQ ID NO:41
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

ATGACCACTG	CGAGAGCCAA	CCAGGGCAAG	ATCCCGGCGA	CCGTCATCAC	CGGCTTCCTC	60
GGCGCCGGCA	AGACGACGAT	GATCCGCAAC	CTGCTGAGA	ACGCCGACGG	CAAGCGCATC	120
GGCCTGATCA	TCAACGAGTT	CGGCGATCTT	GGCGTCGACG	GCGATGTCTT	GAAGGGCTGC	180
GGTGCCGAGG	CCTGCACCGA	GGACGACATC	ATCGAGCTCA	CCAATGGCTG	CATCTGCTGC	240
ACCGTGGCTG	ACGATTTCAT	CCCGACCATG	ACGAAGCTGC	TCGAGCGTGA	AAACCGTCCT	300
GACCACATCA	TCATCGAAAC	CTCGGGCTT	GCCCTGCCGC	AGCCGCTGAT	CGCCGCTTTC	360
AACTGGCCGG	ATATCCGCAAG	CGAAGTGACC	GTCGATGGCG	TCGTCACCGT	GGTCGACAGC	420
GCCGCCGTTG	CCGCTGGCCG	CTTGCCGAC	GACCACGACA	AGGTCGATGC	GCTGCGCGTC	480
GAGGACGACA	ATCTCGATCA	CGAAAGCCCG	ATCGAGGAGC	TGTTGAGGA	TCAACTGACG	540
GCTGCCGATC	TCATCGTTCT	CAACAAGACC	GATCTGATCG	ATGCCCTCCGG	CCTCAAGGCC	600
GTGCGCGACG	AGGTGTCTTC	GCGCACCAAGC	CGCAAGCCA	CGATGATCGA	GGCGAAAAAC	660
GGCGAAGTCG	CGCTGCCAT	CCTGCTTGGC	CTCGGTGTCG	GCACGGAAAG	CGATATGCC	720
AACCGCAAGT	CGCATCACGA	GATGGAGCAC	GAGGCAGGGT	AGGAGCACGA	TCACGACGAG	780
TTCGACAGCT	TCGTCGTCGA	GCTCGGTTCG	ATCGCCGATC	CGGGCGCCTT	CATCGATCGC	840
CTGAAGGGCG	TAATCGCGGA	GCACCGACGGT	CTGCGCCTCA	AGGGTTTGC	AGACGTGCC	900
GGCAAGCCGA	TGCGCCTCCT	GATCCAGGCG	GTCGGCGCCC	GCATCGACCA	ATATTACGAC	960
CGCGCCTGGG	GGCCTGGCGA	AAAGCGCGGT	ACGCGCCTCG	TCGTCATCGG	CCTGCACGAC	1020
ATGGACGAGG	CGGCGGTGCG	CGCCCGCATC	ACCGCGCTCG	TGTAG		1065

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 354 amino acids
  - (B) TYPE: Amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas denitrificans*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBW
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Met Thr Thr Ala Arg Ala Asn Gln Gly Lys Ile Pro Ala Thr Val Ile  
1 5 10 15  
Thr Gly Phe Leu Gly Ala Gly Lys Thr Thr Met Ile Arg Asn Leu Leu  
20 25 30  
Gln Asn Ala Asp Gly Lys Arg Ile Gly Leu Ile Ile Asn Glu Phe Gly  
35 40 45  
Asp Leu Gly Val Asp Gly Asp Val Leu Lys Gly Cys Gly Ala Glu Ala  
50 55 60  
Cys Thr Glu Asp Asp Ile Ile Glu Leu Thr Asn Gly Cys Ile Cys Cys  
65 70 75 80  
Thr Val Ala Asp Asp Phe Ile Pro Thr Met Thr Lys Leu Leu Glu Arg  
85 90 95  
Glu Asn Arg Pro Asp His Ile Ile Ile Glu Thr Ser Gly Leu Ala Leu  
100 105 110  
Pro Gln Pro Leu Ile Ala Ala Phe Asn Trp Pro Asp Ile Arg Ser Glu  
115 120 125  
Val Thr Val Asp Gly Val Val Thr Val Val Asp Ser Ala Ala Val Ala  
130 135 140  
Ala Gly Arg Phe Ala Asp Asp His Asp Lys Val Asp Ala Leu Arg Val  
145 150 155 160  
Glu Asp Asp Asn Leu Asp His Glu Ser Pro Ile Glu Glu Leu Phe Glu  
165 170 175  
Asp Gln Leu Thr Ala Ala Asp Leu Ile Val Leu Asn Lys Thr Asp Leu  
180 185 190  
Ile Asp Ala Ser Gly Leu Lys Ala Val Arg Asp Glu Val Ser Ser Arg  
195 200 205  
Thr Ser Arg Lys Pro Thr Met Ile Glu Ala Lys Asn Gly Glu Val Ala  
210 215 220  
Ala Ala Ile Leu Leu Gly Leu Gly Val Gly Thr Glu Ser Asp Ile Ala  
225 230 235 240  
Asn Arg Lys Ser His His Glu Met Glu His Glu Ala Gly Glu Glu His  
245 250 255  
Asp His Asp Glu Phe Asp Ser Phe Val Val Glu Leu Gly Ser Ile Ala  
260 265 270  
Asp Pro Ala Ala Phe Ile Asp Arg Leu Lys Gly Val Ile Ala Glu His  
275 280 285  
Asp Val Leu Arg Leu Lys Gly Phe Ala Asp Val Pro Gly Lys Pro Met  
290 295 300

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Arg Leu Leu Ile Gln Ala Val Gly Ala Arg Ile Asp Gln Tyr Tyr Asp  
305 310 315 320  
Arg Ala Trp Gly Ala Gly Glu Lys Arg Gly Thr Arg Leu Val Val Ile  
325 330 335  
Gly Leu His Asp Met Asp Glu Ala Ala Val Arg Ala Ala Ile Thr Ala  
340 345 350  
Leu Val

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3828 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobN
- (B) LOCATION: 5060-8887 bp of SEQ ID NO:41
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ATGCATCTGC	TTCTCGCCA	GAAAGGAACG	ATCGCCGACG	GCAACGAGGC	GATCGACCTT	60
GGGAAACGC	CGGCCGATAT	CCTTTCTA	TCGGCCGCCG	ACACCGAGCT	CTCCTCGATC	120
GCCGCGGCTC	ACGGCCGACG	CGACGGAGGC	TTGAGCCTGC	GCATCGCCAG	CCTGATGAGC	180
CTGATGCACC	CGATGTCGGT	CGACACTTAC	GTCGAGCGCA	CGGCGCGTC	CGCCAAGCTG	240
ATCGTCGTCC	GGCCGCTCGG	TGGGCCAGC	TATTTCCGTT	ATCTGCTGGA	AGCCCTGCAT	300
GCGGCTGCCG	TCACCCATCG	TTTCGAGATC	GCGGTTCTGC	CGGGTGAAGA	CAAGCCGGAT	360
CCGGGGCTGG	AGCCTTCTC	CACCGTCGCA	GCCGACGACC	GCCAGCGCCT	TTGGGCTTAC	420
TTCACCGAAG	GCGGCTCGGA	CAATGCCGGG	CTGTTTCTCG	ACTATGCGGC	CGCACTGGTC	480
ACAGGTGCGG	AGAAGCCGCA	GCCGCGAAAG	CCCCTGTTGA	AGGCCGGCAT	CTGGTGGCCG	540
GGTGTGGGTG	TGATCGGCGT	CAGCGAATGG	CAGTCCCTTG	TTCAGGGACG	GATGGTAGCG	600
AGGGAGGGAT	TCGAACCCCCC	GACGGTCGGG	ATCTGTTTT	ACCGCGCGCT	CGTGCAGAGT	660
GGCGAGACAC	GGCCTGTGGA	GGCGCTGATC	GATGCGCTGG	AGGCTGAAGG	TGTGCGGGCA	720
CTGCGCGTGT	TTGTCTCAAG	CCTCAAGGAT	GCCGTTTCCG	TCGGCACGCT	GCAGGGCGATT	780
TTTTCGAGG	CCGCACCCCGA	CGTGGTGTATG	AACGCCACTG	GCTTTCGCGT	CTCGTCGCC	840
GGTGCCGACC	GTCAGCCGAC	GGTGTCTGGAA	TCGACCGGTG	CGCCGGTGCT	GCAGGGTATT	900
TTCTCCGGCT	CGTCGCGGGGC	GCAATGGGAA	ACGTCGCCG	AGGGGCTGAT	GGCGCGCGAC	960
CTCGCCATGA	ACGTGGCACT	CCCCGAAGTC	GATGGCCGCA	TCCTTGCAGC	CGCCGCTCTCC	1020
TTCAAGGCGG	CGTCGATCTA	TGACGCCAAG	GTGGAGGCCA	ATATCGTCGG	CCATGAGCCG	1080
CTCGAAGGCC	GGGTGCGCTT	TGCCGCTGAT	CTTGCCGTC	ACTGGGCGAA	CGTGCGCCGG	1140
GCAGAGCCCCG	CCGAGCGCCG	TATTGCCATC	GTCATGGCCA	ACTATCCGAA	CCGCGACGGT	1200
CGCCTCGGCA	ACGGTGTGG	GCTCGACACG	CCGGCCGGTA	CCGTCGAGGT	GCTTAGCGCC	1260
ATGGCGCGGG	AAGGCTATGC	GGTCGGTGTAG	GTTCCCGCCG	ATGGCGACGC	GCTGATCCGC	1320
TTTCTGATGG	CCGGGCGGAC	CAATGCGGCG	AGCCATGACC	GTGAAATCCG	CGAGCGTATT	1380

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TCGCTGAACG	ATTACAAAAC	GTTCTTCGAT	TCGCTTCGA	AACAGATAAA	GGATGAAGTT	1440
GCGGTCGCT	GGGGCGTGCC	GGAGGCCGAT	CCCTTTTCC	TCGATGGCGC	CTTCGCGCTG	1500
CCGCTCGCCC	GCTTCGGCGA	GGTGATCGTC	GGCATCCAAC	CGGCGCGCGG	CTACAACATC	1560
GATCCGAAGG	AAAGCTACCA	TTCCCCGGAC	CTCGTGCCTG	CGCATGGCTA	TCTGCCCTTC	1620
TACGCCCTCC	TGCGCCAGCA	GTTCGGAGCG	CAGGCGATCG	TCCACATGGG	CAAGCACGGC	1680
AATCTCGAAT	GGCTGCCGGG	CAAGGCGCTG	GCGCTGTCGG	AAACCTGCTA	TCCCGAAGCG	1740
ATCTTCGGGC	CGCTGCCGCA	CATCTATCCC	TTCATCGTCA	ACGATCCGGG	CGAAGGTACG	1800
CAGGCCAAGC	GCCGACCCAG	CGCCGTCATC	ATCGACCAC	TGACCCCGCC	CTTGACCGCG	1860
GCCGAATCCT	ACGGCCCGCT	CAAGGATCTG	GAAGCGCTG	TCGACGAATA	TTACGACGCC	1920
GCCGGCGGTG	ATCCCGCCTG	CCTCAGGCTG	CTCAGCCGCC	AGATCCTCGA	TCTCGTGC	1980
GACATCGGCC	TCGACAGCGA	CGCAGGCATC	GACAGGGCG	ACAGCGACGA	CAAGGCCTG	2040
GAAAAGCTCG	ACGCCTATCT	CTGCGACCTC	AAGGAAATGC	AGATCCGCGA	CGGCCCTGCAC	2100
ATCTTCGGCG	TTGCGCCGGA	AGGGCGGTTG	TTGACGGACC	TCACCGTAGC	GCTGGCGCGC	2160
GTGCCCGAG	GTCTCGCGA	GGGCGGCAC	CAGAGCCTG	AGCGGGCGAT	CGCAGCGGAT	2220
GCGGGGCTGC	GTGGGTTTC	TATCCCCACC	TCGGCGGGGG	GCAACCCCGC	ACCGGACGCC	2280
CAACCCCTCG	ACCCGCTCGA	CTGCGTCATG	TCCGACACCT	GGACAGGCC	GAAACCGTCC	2340
ATCCTCGCTG	ACCTCTCGGA	CGCCCCCTGG	CGCACCGCCG	CGGATACGGT	CGAGCGCATC	2400
GAGTTGCTTG	CCGCAAATCT	CGTGTGGGT	GAACCTGGCTT	GCCCCGACCA	CTGGGCCAAC	2460
ACCCCGCCG	TGCTCGCGA	AATCGAAACG	CGCCTGAAGC	CGTCGATTTC	AAACTCGGGT	2520
GCGCCGAGA	TGACCGGCTT	CCTCACCGGT	CTCAGCGGCC	GCTTCGTCG	CCCCGGTCCA	2580
TCGGGGCGCG	CGACGCGCGG	CCGGCGGGAT	GTGTTGCCGA	CGGGGGCGAA	TTTCTACTCG	2640
GTCGACAGCC	GCGCCGTGCC	GACGCCGGCG	GCTTACGAGC	TTGGAAGAA	ATCGGCCGAG	2700
CTTCTGATCC	GCGCTACCT	GCAGGACCAT	GGCGAATGGC	CGTCCTCCTT	TGGCCTGACC	2760
GCCTGGGCA	CGCGAACAT	GCGCACCGGC	GGCGACGACA	TGCCCCAGGC	CCTGGCGCTG	2820
ATCGGCGCCA	AGCCCACCTG	GGACATGGTC	TCTCGCCGGG	TGATGGGCTA	CGAGATCGT	2880
CCGCTCGCAG	TCCTCGGCCG	CCCACGCGTC	GACGTGACCT	TGCGCATTTC	CGGCTTCTTC	2940
CGCGATGCCT	TCCCGGACCA	GATCGCGCTC	TTCGACAAGG	CGATCCGCGC	CGTCGCGCTG	3000
GAGGAAGACG	ATGCCGACAA	CATGATCGCC	GCACGCATGC	GGGGGGAAAG	CCGGCGGCTG	3060
GAGGCCGAAG	GCGTGGAAAGC	CGCCGAGGCC	GGCGCTCGCG	CCTCTTACCG	CGTCTTTGGC	3120
GCAAAGCCCC	GTGCTATGG	CGCCGCCCTG	CAGGCCTGTA	TCGACGAGAA	GGGCTGGGAA	3180
ACCAAAGCAG	ATCTCGCGA	GGCCTATCTT	ACCTGGGGCG	CCTATGCC	TGGGCCCGC	3240
GAGGAGGGCA	AGGCCGAGCG	CGATCTTTTC	GAGGAGCGCC	TGCGCACGAT	AGAGGCGGTG	3300
GTGCAAAACC	AGGACAACCG	CGAGCACGAT	CTGCTCGACA	GCGACGACTA	CTACCACTTC	3360
GAAGGCGGC	TGAGCGCTGC	CGCCGAACAG	CTCGCGGTC	ACCGTCCGGC	GATCTACCAC	3420
AACGACCATT	CCCCTCCGGA	AAAGCCTGTG	ATCCGGTCG	TCGAAGAAGA	GATCGGCCGC	3480
GTGGTCCGGG	CCCGCGTCGT	CAATCCCAAG	TGGATCGATG	CGCTCATGCG	CCACGGATAC	3540
AAGGGCGCCT	TCGAGATCGC	TGCCACGGTC	GACTACATGT	TGCCCCTTGC	CGCGACCAACG	3600
GGTGGCGGTGC	GGCACCATCA	TTTCGAGGCC	GCTTATCAGG	CGTTCATTTGT	CGACGAGCGC	3660
GTGGCTGACT	TCATCGCGA	CAAGAACCCG	GCCGCCTT	CCGAGCTTGC	CGAACGCC	3720
CTTGAAGCAA	TCGACCGCAA	TCTCTGGACG	CCGCGCTCGA	ATTCCGGCGCG	GTTTGAACCTT	3780
GCGGCATCG	GCACGGCAGC	AACCCGGCTT	CGTGCCTGCA	ATGAATAG		3828

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1275 amino acids
  - (B) TYPE: Amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas denitrificans*
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE:
  - (H) CELL LINE:

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(I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBN
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO:48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Met His Leu Leu Leu Ala Gln Lys Gly Thr Ile Ala Asp Gly Asn Glu  
1 5 10 15  
Ala Ile Asp Leu Gly Gln Thr Pro Ala Asp Ile Leu Phe Leu Ser Ala  
20 25 30  
Ala Asp Thr Glu Leu Ser Ser Ile Ala Ala Ala His Gly Arg Arg Asp  
35 40 45  
Gly Gly Leu Ser Leu Arg Ile Ala Ser Leu Met Ser Leu Met His Pro  
50 55 60  
Met Ser Val Asp Thr Tyr Val Glu Arg Thr Ala Arg His Ala Lys Leu  
65 70 75 80  
Ile Val Val Arg Pro Leu Gly Gly Ala Ser Tyr Phe Arg Tyr Leu Leu  
85 90 95  
Glu Ala Leu His Ala Ala Ala Val Thr His Arg Phe Glu Ile Ala Val  
100 105 110  
Leu Pro Gly Asp Asp Lys Pro Asp Pro Gly Leu Glu Pro Phe Ser Thr  
115 120 125  
Val Ala Ala Asp Asp Arg Gln Arg Leu Trp Ala Tyr Phe Thr Glu Gly  
130 135 140  
Gly Ser Asp Asn Ala Gly Leu Phe Leu Asp Tyr Ala Ala Ala Leu Val  
145 150 155 160  
Thr Gly Ala Glu Lys Pro Gln Pro Ala Lys Pro Leu Leu Lys Ala Gly  
165 170 175  
Ile Trp Trp Pro Gly Ala Gly Val Ile Gly Val Ser Glu Trp Gln Ser  
180 185 190  
Leu Val Gln Gly Arg Met Val Ala Arg Glu Gly Phe Glu Pro Pro Thr  
195 200 205  
Val Gly Ile Cys Phe Tyr Arg Ala Leu Val Gln Ser Gly Glu Thr Arg  
210 215 220  
  
Pro Val Glu Ala Leu Ile Asp Ala Leu Glu Ala Glu Gly Val Arg Ala  
225 230 235 240  
Leu Pro Val Phe Val Ser Ser Leu Lys Asp Ala Val Ser Val Gly Thr  
245 250 255  
Leu Gln Ala Ile Phe Ser Glu Ala Ala Pro Asp Val Val Met Asn Ala  
260 265 270  
Thr Gly Phe Ala Val Ser Ser Pro Gly Ala Asp Arg Gln Pro Thr Val  
275 280 285  
Leu Glu Ser Thr Gly Ala Pro Val Leu Gln Val Ile Phe Ser Gly Ser  
290 295 300  
Ser Arg Ala Gln Trp Glu Thr Ser Pro Gln Gly Leu Met Ala Arg Asp  
305 310 315 320  
Leu Ala Met Asn Val Ala Leu Pro Glu Val Asp Gly Arg Ile Leu Ala  
325 330 335  
Arg Ala Val Ser Phe Lys Ala Ala Ser Ile Tyr Asp Ala Lys Val Glu  
340 345 350  
Ala Asn Ile Val Gly His Glu Pro Leu Glu Gly Arg Val Arg Phe Ala  
355 360 365  
Ala Asp Leu Ala Val Asn Trp Ala Asn Val Arg Arg Ala Glu Pro Ala  
370 375 380  
Glu Arg Arg Ile Ala Ile Val Met Ala Asn Tyr Pro Asn Arg Asp Gly  
385 390 395 400  
Arg Leu Gly Asn Gly Val Gly Leu Asp Thr Pro Ala Gly Thr Val Glu

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405	410	415
Val Leu Ser Ala Met Ala Arg Glu Gly Tyr Ala Val Gly Glu Val Pro		
420	425	430
Ala Asp Gly Asp Ala Leu Ile Arg Phe Leu Met Ala Gly Pro Thr Asn		
435	440	445
Ala Ala Ser His Asp Arg Glu Ile Arg Glu Arg Ile Ser Leu Asn Asp		
450	455	460
Tyr Lys Thr Phe Phe Asp Ser Leu Pro Lys Gln Ile Lys Asp Glu Val		
465	470	475
Ala Gly Arg Trp Gly Val Pro Glu Ala Asp Pro Phe Phe Leu Asp Gly		
485	490	495
Ala Phe Ala Leu Pro Leu Ala Arg Phe Gly Glu Val Ile Val Gly Ile		
500	505	510
Gln Pro Ala Arg Gly Tyr Asn Ile Asp Pro Lys Glu Ser Tyr His Ser		
515	520	525
Pro Asp Leu Val Pro Pro His Gly Tyr Leu Ala Phe Tyr Ala Phe Leu		
530	535	540
Arg Gln Gln Phe Gly Ala Gln Ala Ile Val His Met Gly Lys His Gly		
545	550	555
Asn Leu Glu Trp Leu Pro Gly Lys Ala Leu Ala Leu Ser Glu Thr Cys		
565	570	575
Tyr Pro Glu Ala Ile Phe Gly Pro Leu Pro His Ile Tyr Pro Phe Ile		
580	585	590
Val Asn Asp Pro Gly Glu Gly Thr Gln Ala Lys Arg Arg Thr Ser Ala		
595	600	605
Val Ile Ile Asp His Leu Thr Pro Pro Leu Thr Arg Ala Glu Ser Tyr		
610	615	620
Gly Pro Leu Lys Asp Leu Glu Ala Leu Val Asp Glu Tyr Tyr Asp Ala		
625	630	635
Ala Gly Gly Asp Pro Arg Arg Leu Arg Leu Leu Ser Arg Gln Ile Leu		
645	650	655
Asp Leu Val Arg Asp Ile Gly Leu Asp Ser Asp Ala Gly Ile Asp Arg		
660	665	670
Gly Asp Ser Asp Asp Lys Ala Leu Glu Lys Leu Asp Ala Tyr Leu Cys		
675	680	685
Asp Leu Lys Glu Met Gln Ile Arg Asp Gly Leu His Ile Phe Gly Val		
690	695	700
Ala Pro Glu Gly Arg Leu Leu Thr Asp Leu Thr Val Ala Leu Ala Arg		
705	710	715
Val Pro Arg Gly Leu Gly Glu Gly Asp Gln Ser Leu Gln Arg Ala		
725	730	735
Ile Ala Ala Asp Ala Gly Leu Arg Gly Phe Ala Ile Pro Thr Ser Ala		
740	745	750
Gly Gly Asn Pro Ala Arg Asp Ala Gln Pro Phe Asp Pro Leu Asp Cys		
755	760	765
Val Met Ser Asp Thr Trp Thr Gly Pro Lys Pro Ser Ile Leu Ala Asp		
770	775	780
Leu Ser Asp Ala Pro Trp Arg Thr Ala Gly Asp Thr Val Glu Arg Ile		
785	790	795
Glu Leu Leu Ala Ala Asn Leu Val Ser Gly Glu Leu Ala Cys Pro Asp		
805	810	815
His Trp Ala Asn Thr Arg Ala Val Leu Gly Glu Ile Glu Thr Arg Leu		
820	825	830
Lys Pro Ser Ile Ser Asn Ser Gly Ala Ala Glu Met Thr Gly Phe Leu		
835	840	845
Thr Gly Leu Ser Gly Arg Phe Val Ala Pro Gly Pro Ser Gly Ala Pro		
850	855	860
Thr Arg Gly Arg Pro Asp Val Leu Pro Thr Gly Arg Asn Phe Tyr Ser		
865	870	875
Val Asp Ser Arg Ala Val Pro Thr Pro Ala Ala Tyr Glu Leu Gly Lys		
885	890	895
Lys Ser Ala Glu Leu Leu Ile Arg Arg Tyr Leu Gln Asp His Gly Glu		

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900	905	910
Trp Pro Ser Ser Phe Gly Leu Thr Ala Trp Gly Thr Ala Asn Met Arg		
915	920	925
Thr Gly Gly Asp Asp Ile Ala Gln Ala Leu Ala Leu Ile Gly Ala Lys		
930	935	940
Pro Thr Trp Asp Met Val Ser Arg Arg Val Met Gly Tyr Glu Ile Val		
945	950	955
Pro Leu Ala Val Leu Gly Arg Pro Arg Val Asp Val Thr Leu Arg Ile		
965	970	975
Ser Gly Phe Phe Arg Asp Ala Phe Pro Asp Gln Ile Ala Leu Phe Asp		
980	985	990
Lys Ala Ile Arg Ala Val Ala Leu Glu Glu Asp Asp Ala Asp Asn Met		
995	1000	1005
Ile Ala Ala Arg Met Arg Ala Glu Ser Arg Arg Leu Glu Ala Glu Gly		
1010	1015	1020
Val Glu Ala Ala Glu Ala Ala Arg Arg Ala Ser Tyr Arg Val Phe Gly		
1025	1030	1035
Ala Lys Pro Gly Ala Tyr Gly Ala Ala Leu Gln Ala Leu Ile Asp Glu		
1045	1050	1055
Lys Gly Trp Glu Thr Lys Ala Asp Leu Ala Glu Ala Tyr Leu Thr Trp		
1060	1065	1070
Gly Ala Tyr Ala Tyr Gly Ala Gly Glu Glu Gly Lys Ala Glu Arg Asp		
1075	1080	1085
Leu Phe Glu Glu Arg Leu Arg Thr Ile Glu Ala Val Val Gln Asn Gln		
1090	1095	1100
Asp Asn Arg Glu His Asp Leu Leu Asp Ser Asp Asp Tyr Tyr Gln Phe		
1105	1110	1115
Glu Gly Gly Met Ser Ala Ala Ala Glu Gln Leu Gly Gly His Arg Pro		
1125	1130	1135
Ala Ile Tyr His Asn Asp His Ser Arg Pro Glu Lys Pro Val Ile Arg		
1140	1145	1150
Ser Leu Glu Glu Glu Ile Gly Arg Val Val Arg Ala Arg Val Val Asn		
1155	1160	1165
Pro Lys Trp Ile Asp Gly Val Met Arg His Gly Tyr Lys Gly Ala Phe		
1170	1175	1180
Glu Ile Ala Ala Thr Val Asp Tyr Met Phe Ala Phe Ala Ala Thr Thr		
1185	1190	1195
Gly Ala Val Arg Asp His His Phe Glu Ala Ala Tyr Gln Ala Phe Ile		
1205	1210	1215
Val Asp Glu Arg Val Ala Asp Phe Met Arg Asp Lys Asn Pro Ala Ala		
1220	1225	1230
Phe Ala Glu Leu Ala Glu Arg Leu Leu Glu Ala Ile Asp Arg Asn Leu		
1235	1240	1245
Trp Thr Pro Arg Ser Asn Ser Ala Arg Phe Glu Leu Ala Gly Ile Gly		
1250	1255	1260
Thr Ala Ala Thr Arg Leu Arg Ala Gly Asn Glu		
1265	1270	1275

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 645 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ORIGINAL SOURCE:
  - (A) ORGANISM: Pseudomonas denitrificans

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- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: cobo
- (B) LOCATION: 9034-9678 bp of SEQ ID NO:41
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

ATGAGCGACG	AGACGACAGT	AGGCGGCGAA	GCCCCGGCCG	AGAAGGACGA	TGCCC GCCAC	60
GCCATGAAGA	TGGCGAAGAA	GAAGGCAGCA	CGCGAAAAGA	TCATGGCGAC	GAAGACCGAC	120
GAGAAGGGTC	TGATCATCGT	CAACACCGGC	AAAGGCAAGG	GCAAGTCGAC	CGCCGGCTTC	180
GGCATGATCT	TCCGCCATAT	CGCCCACGGC	ATGCCCTGCG	CCGTCGTGCA	GTTCATCAAG	240
GGTGCATGG	CAACCGCGA	GCGCGAGTTG	ATCGAGAACG	ATTCGGCGA	TGTCTGCCAG	300
TTCTACACGC	TCGGCGAGGG	CTTCACCTGG	GAAACGCGAG	ATCGCGCCCG	CGATGTTGCG	360
ATGGCTGAAA	AGGCCTGGG	GAAGGCGAAG	GAACGTGATCC	GTGACGAGCG	CAACTCGATG	420
GTGCTGCTCG	ACGAGATCAA	CATTGCTCTG	CGCTACGACT	ACATCGACGT	CGCCGAAGTG	480
GTGCGCTTCC	TGAAGGAAGA	AAAGCCGCAC	ATGACGCATG	TGGTGCTCAC	CGGCCGCAAC	540
GCGAAAGAAG	ACCTGATCGA	AGTCGCCGAT	CTCGTCACTG	AGATGGAGCT	GATCAAGCAT	600
CCGTTCCGTT	CCGGCATCAA	GGCGCAGCAG	GGCGTGGAGT	TCTGA		645

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acid
- (B) TYPE: Amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas denitrificans
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: COBO
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Translation product of SEQ ID NO: 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Met Ser Asp Glu Thr Thr Val Gly Gly Glu Ala Pro Ala Glu Lys Asp  
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1 Asp Ala Arg His Ala Met Lys Met Ala Lys Lys Ala Ala Arg Glu  
 5 20 25 30 35 40 45 50 55 60  
 Lys Ile Met Ala Thr Lys Thr Asp Glu Lys Gly Leu Ile Ile Val Asn  
 10 15 20 25 30 35 40 45 50 55 60  
 Thr Gly Lys Gly Lys Ser Thr Ala Gly Phe Gly Met Ile Phe  
 15 20 25 30 35 40 45 50 55 60  
 Arg His Ile Ala His Gly Met Pro Cys Ala Val Val Gln Phe Ile Lys  
 20 25 30 35 40 45 50 55 60 65 70 75 80  
 Gly Ala Met Ala Thr Gly Glu Arg Glu Leu Ile Glu Lys His Phe Gly  
 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95  
 Asp Val Cys Gln Phe Tyr Thr Leu Gly Glu Gly Phe Thr Trp Glu Thr  
 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110  
 Gln Asp Arg Ala Arg Asp Val Ala Met Ala Glu Lys Ala Trp Glu Lys  
 35 40 45 50 55 60 65 70 75 80 85 90 95 115 120 125  
 Ala Lys Glu Leu Ile Arg Asp Glu Arg Asn Ser Met Val Leu Leu Asp  
 40 45 50 55 60 65 70 75 80 85 90 95 130 135 140  
 Glu Ile Asn Ile Ala Leu Arg Tyr Asp Tyr Ile Asp Val Ala Glu Val  
 45 50 55 60 65 70 75 80 85 90 95 145 150 155 160  
 Val Arg Phe Leu Lys Glu Glu Lys Pro His Met Thr His Val Val Leu  
 50 55 60 65 70 75 80 85 90 95 165 170 175  
 Thr Gly Arg Asn Ala Lys Glu Asp Leu Ile Glu Val Ala Asp Leu Val  
 55 60 65 70 75 80 85 90 95 180 185 190  
 Thr Glu Met Glu Leu Ile Lys His Pro Phe Arg Ser Gly Ile Lys Ala  
 60 65 70 75 80 85 90 95 195 200 205  
 Gln Gln Gly Val Glu Phe  
 65 70 75 80 85 90 95 210

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanobacterium ivanovii*
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: containing *corA* or *sumT* gene
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Nucleotide Sequence of the 5' to 3' strand from the 955 bp fragment of *Methanobacterium ivanovii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

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CCAGGAGATC	CCGAACTTAT	CACTCTCAA	GCTGTAAACG	TGTAAAAAAA	AGCGGATGTT	120
GTACTGTACG	ACAAACCTGC	AAATGAAGAA	ATTTTAAAGT	ATGCTGAAGG	TGCAAAACTA	180
ATATATGTCG	AAAAACAAAGC	AGGACATCAT	TACAAATCTC	AAAATGAAAT	CAATACTCTT	240
CTTGTGAAAG	AAGCAAAAGA	AAATGATTTA	GTAGTACGCC	TTAAAGGTGG	AGACCCCTTT	300
GTATTTGGAA	GAGGAGGCGA	GGAAATTCTG	GCCCTTGAG	AAGAAGGAAT	TGATTTGAG	360
TTAGTTCCAG	GGGTAACCTTC	TGCAATTGGA	GTTCCAACAA	CAATTGGGCT	TCCAGTTACT	420
CATAGAGGTG	TTGCAACATC	GTTTACAGTT	GTTACAGGTC	ATGAAGACCC	AACAAAATGC	480
AAGAAACAGG	TAGGATGGGA	CTTTAAAGCA	GATACTATTG	TAATACTTAT	GGGTATTGGA	540
AATTTAGCTG	AAAATACAGC	AGAAATTATG	AAACATAAAAG	ATCCTGAAAC	TCCAGTTGT	600
GTAATTGAAA	ATGGTACGAT	GGAAGGTCAA	AGGATAATAA	CGGGCACACT	GGAAAATATA	660
GCTGAAAGG	ATATTAAACC	TCCTGCTTTA	GTGGTATTGG	AAATGTTGTC	AATGTTTTA	720
AAGAAATGAA	TCAAATCACT	GGCTGATCTA	TTAAGAAGGC	AATATCATGA	ATGGATTAGA	780
AGGTAAAAAA	ATTGTTATAA	CAAGACCTGC	TGAAAGGCT	AAAGACTCA	TTGAAATGGT	840
AAAATCTTAT	GGAGCAGTTC	CAATTGTAAC	TCCTACAATT	GAACTCAAAG	ATTCCAAGCC	900
AGAAGAAGTG	ATAAAATTAT	GTAATATGAT	AAATGAACCT	TGATTGGCCT	TATAT	955

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: Methanobacterium ivanovii
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY: corA or sumT
- (B) LOCATION: 34-729 bp of SEQ ID NO:52
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ATGGTAGTTT	ATTTAGTAGG	TGCGGGTCCA	GGAGATCCCG	AACTTATCAC	TCTCAAAGCT	60
GTAAACGTGT	AAAAAAAAGC	GGATGTTGTA	CTGTACGACA	AACCTGCAAA	TGAAGAAATT	120
TTAAAGTATG	CTGAAGGTGC	AAAACATAAA	TATGTCGAA	AAACAGCAGG	ACATCATTAC	180
AAATCTCAA	ATGAAATCAA	TACTCTTCTT	GTTGAAGAAG	CAAAGAAAAA	TGATTTAGTA	240
GTACGCCCTA	AAGGTGGAGA	CCCCTTGT	TTTGGAAAGAG	GAGGCAGGGA	AATTCTGCC	300
CTTGAGAAG	AGGAATTGA	TTTTGAGTTA	GTTCCAGGGG	TAACCTCTGC	AATTGGAGTT	360
CCAACAACAA	TTGGGCTTCC	AGTTACTCAT	AGAGGTGTTG	CAACATCGTT	TACAGTTGTT	420
ACAGGTATG	AAGACCCAA	AAAATGCAAG	AAACAGGTAG	GATGGGACTT	TAAAGCAGAT	480
ACTATTGTAA	TACTTATGGG	TATTGGAAAT	TTAGCTGAAA	ATACAGCAGA	AATTATGAAA	540
CATAAAGATC	CTGAAACTCC	AGTTTGTGA	ATTGAAAATG	GTACGATGGA	AGGTCAAAGG	600
ATAATAACGG	GCACACTGGA	AAATATAGCT	GGAAAGGATA	TTAACCTCC	TGCTTTAGTG	660
GTATTGGAAA	TGTTGTCAAT	GTTTTAAAG	AAATGA			696

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 231 amino acids  
 (B) TYPE: Amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(iv) ORIGINAL SOURCE:  
 (A) ORGANISM: Methanobacterium ivanovii  
 (B) STRAIN:  
 (C) INDIVIDUAL ISOLATE:  
 (D) DEVELOPMENTAL STAGE:  
 (E) HAPLOTYPE:  
 (F) TISSUE TYPE:  
 (G) CELL TYPE:  
 (H) CELL LINE:  
 (I) ORGANELLE:

(ix) FEATURE:  
 (A) NAME/KEY: CORA  
 (B) LOCATION:  
 (C) IDENTIFICATION METHOD:  
 (D) OTHER INFORMATION: Translation product of SEQ ID NO:53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met Val Val Tyr Leu Val Gly Ala Gly Pro Gly Asp Pro Glu Leu Ile  
 1 5 10 15  
 Thr Leu Lys Ala Val Asn Val Leu Lys Lys Ala Asp Val Val Leu Tyr  
 20 25 30  
 Asp Lys Pro Ala Asn Glu Glu Ile Leu Lys Tyr Ala Glu Gly Ala Lys  
 35 40 45  
 Leu Ile Tyr Val Gly Lys Gln Ala Gly His His Tyr Lys Ser Gln Asn  
 50 55 60  
 Glu Ile Asn Thr Leu Leu Val Glu Glu Ala Lys Glu Asn Asp Leu Val  
 65 70 75 80  
 Val Arg Leu Lys Gly Gly Asp Pro Phe Val Phe Gly Arg Gly Glu  
 85 90 95  
 Glu Ile Leu Ala Leu Val Glu Glu Gly Ile Asp Phe Glu Leu Val Pro  
 100 105 110  
 Gly Val Thr Ser Ala Ile Gly Val Pro Thr Thr Ile Gly Leu Pro Val  
 115 120 125  
 Thr His Arg Gly Val Ala Thr Ser Phe Thr Val Val Thr Gly His Glu  
 130 135 140  
 Asp Pro Thr Lys Cys Lys Lys Gln Val Gly Trp Asp Phe Lys Ala Asp  
 145 150 155 160  
 Thr Ile Val Ile Leu Met Gly Ile Gly Asn Leu Ala Glu Asn Thr Ala  
 165 170 175  
 Glu Ile Met Lys His Lys Asp Pro Glu Thr Pro Val Cys Val Ile Glu  
 180 185 190  
 Asn Gly Thr Met Glu Gly Gln Arg Ile Ile Thr Gly Thr Leu Glu Asn  
 195 200 205  
 Ile Ala Gly Lys Asp Ile Lys Pro Pro Ala Leu Val Val Leu Glu Met  
 210 215 220  
 Leu Ser Met Phe Leu Lys Lys  
 225 230

## (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

## (ii) MOLECULE TYPE: polypeptide

## (iii) HYPOTHETICAL: No

## (iv) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

## (ix) FEATURE:

- (A) NAME/KEY: fragment of cysG protein
- (B) LOCATION: amino acids 204-460
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Glu Gln Leu Ile Asn Glu Pro Leu Asp His Arg Gly Glu Val Val Leu  
 5 10 15  
 val Gly Ala Gly Pro Gly Asp Ala Gly Leu Leu Thr Leu Lys Gly Leu  
 20 25 30  
 Gln Gln Ile Gln Gln Ala Asp Val Val Val Tyr Asp Arg Leu Val Ser  
 35 40 45  
 Asp Asp Ile Met Asn Leu Val Arg Arg Asp Ala Asp Arg Val Phe Val  
 50 55 60  
 Gly Lys Arg Ala Gly Tyr His Cys Val Pro Gln Glu Glu Ile Asn Gln  
 65 70 75 80  
 Ile Leu Leu Arg Glu Ala Gln Lys Gly Lys Arg Val Val Arg Leu Lys  
 85 90 95  
 Gly Gly Asp Pro Phe Ile Phe Gly Arg Gly Glu Glu Leu Glu Thr  
 100 105 110  
 Leu Cys Asn Ala Gly Ile Pro Phe Ser Val Val Pro Gly Ile Thr Ala  
 115 120 125  
 Ala Ser Gly Cys Ser Ala Tyr Ser Gly Ile Pro Leu Thr His Arg Asp  
 130 135 140  
 Tyr Ala Gln Ser Val Arg Leu Ile Thr Gly His Leu Lys Thr Gly Gly  
 145 150 155 160  
 Glu Leu Asp Trp Glu Asn Leu Ala Ala Glu Lys Gln Thr Leu Val Phe  
 165 170 175  
 Tyr Met Gly Leu Asn Gln Ala Ala Thr Ile Gln Gln Lys Leu Ile Glu  
 180 185 190  
 His Gly Met Pro Gly Glu Met Pro Val Ala Ile Val Glu Asn Gly Thr  
 195 200 205  
 Ala Val Thr Gln Arg Val Ile Asp Gly Thr Leu Thr Gln Leu Gly Glu  
 210 215 220  
 Leu Ala Gln Gln Met Asn Ser Pro Ser Leu Ile Ile Ile Gly Arg Val  
 225 230 235 240  
 Val Gly Leu Arg Asp Lys Leu Asn Trp Phe Ser

10724598  
245 250

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: fragment of sumT gene
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

CGCGGAATTC CCNGGNGAYC CNGARCT

27

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: fragment of sumT gene
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CGCGGAATTC GTRTAYCTWG TDGGWGC

27

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: fragment of sumT gene
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

10724598  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CGCGAAGCTT RTTYTCWAGD GTNCC

25

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Oligonucleotide

(ix) FEATURE:  
(A) NAME/KEY: fragment of sumT gene  
(B) LOCATION: -12 - 15  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: as seen in specification, p. 182,

line 5.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGCCGAATTC ATATGGTAGT TTATTTA

27

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Oligonucleotide

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: As seen in specification on p. 182,  
line 10. Hybrid fragment complementary strand derived from sumT gene  
sequence.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GGCCGAGCTC TATTACATAA TT

220